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SEQUENCE LISTING

TECH CENTER 1600/2900

1

<110> Young, Robert

<120> Compounds for Targeting

<130> 43191-256808

<140> US 09/825,012

<141> 2001-04-03

<150> US 60/237,159

<151> 2000-10-02

A35  
<150> GB 0008049.9

<151> 2000-04-03

<160> 101

<170> PatentIn version 3.1

<210> 1

<211> 282

<212> PRT

<213> Homo sapiens

<400> 1

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1 5 10 15

Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr  
20 25 30

Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val  
35 40 45

Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp  
50 55 60

Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp  
65 70 75 80

Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn  
85 90 95

Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser  
100 105 110

Ala Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn  
115 120 125

Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe  
130 135 140

Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly  
145 150 155 160

Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val  
165 170 175

Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn  
180 185 190

Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu  
195 200 205

Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr  
210 215 220

Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly  
225 230 235 240

Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn  
245 250 255

Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser  
260 265 270

Asp His Tyr Pro Val Glu Val Met Leu Lys

275

280

&lt;210&gt; 2

&lt;211&gt; 1039

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

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cattctcgac atctctgagg acatcaccat catctcagga tgaggggcat gaagctgctg	180
ggggcgctgc tggcactggc ggccctactg cagggggccg tgtccctgaa gatcgccagcc	240
ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt	300
gtgcagatcc tgagccgcta tgacatcgcc ctggtccagg aggtcagaga cagccacctg	360
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gttcccgact cggctttcc cttaacttc caggctgcct atggcctgag tgaccaactg	960
gcccaaggcca tcagtgacca ctatccagtg gaggtgatgc tgaagtgagc agcccctccc	1020
cacaccagtt gaactgcag	1039

&lt;210&gt; 3

&lt;211&gt; 260

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	Thr	Phe	Gly	Glu	Thr	Lys	Met
1				5				10						15	

Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	Gln	Ile	Leu	Ser	Arg	Tyr
				20				25					30		

Asp	Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	Asp	Ser	His	Leu	Thr	Ala	Val
					35			40			45				

Gly	Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	Asp	Ala	Pro	Asp	Thr	Tyr	His
					50			55			60				

Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	Asn	Ser	Tyr	Lys	Glu	Arg	Tyr
					65			70			75		80		

Leu	Phe	Val	Tyr	Arg	Pro	Asp	Gln	Val	Ser	Ala	Val	Asp	Ser	Tyr	Tyr
					85				90			95			

Tyr	Asp	Asp	Gly	Cys	Glu	Pro	Cys	Gly	Asn	Asp	Thr	Phe	Asn	Arg	Glu
					100			105					110		

Pro	Ala	Ile	Val	Arg	Phe	Phe	Ser	Arg	Phe	Thr	Glu	Val	Arg	Glu	Phe
					115			120			125				

Ala	Ile	Val	Pro	Leu	His	Ala	Ala	Pro	Gly	Asp	Ala	Val	Ala	Glu	Ile
					130			135			140				

Asp	Ala	Leu	Tyr	Asp	Val	Tyr	Leu	Asp	Val	Gln	Glu	Lys	Trp	Gly	Leu
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Glu	Asp	Val	Met	Leu	Met	Gly	Asp	Phe	Asn	Ala	Gly	Cys	Ser	Tyr	Val
					165				170			175			

Arg	Pro	Ser	Gln	Trp	Ser	Ser	Ile	Arg	Leu	Trp	Thr	Ser	Pro	Thr	Phe
					180			185			190				

Gln	Trp	Leu	Ile	Pro	Asp	Ser	Ala	Asp	Thr	Thr	Ala	Thr	Pro	Thr	His
					195			200			205				

Cys	Ala	Tyr	Asp	Arg	Ile	Val	Val	Ala	Gly	Met	Leu	Leu	Arg	Gly	Ala
					210			215			220				

Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly  
 225 230 235 240

Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val Glu  
 245 250 255

Val Met Leu Lys  
 260

<210> 4

<211> 783

<212> DNA

<213> Homo sapiens

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 agagacagcc acctgactgc cgtgggaaag ctgctggaca acctaataca ggacgcacca 180  
 gacacctatc actacgttgtt cagttagcca ctgggacgga acagctataaa ggagcgctac 240  
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 gtagccgaga tcgacgctct ctatgacgtc tacctggatg tccaaagagaa atggggcttg 480  
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 gacaccacag ctacacccac gcactgtgcc tatgacagga tcgtggttgc agggatgctg 660  
 ctccgagggg ccgttgcatttgc cgactcggtt cttccctta acttccaggc tgcctatggc 720  
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<210> 5

<211> 161

<212> PRT

291  
2183  
3151  
3151

<213> Homo sapiens

<400> 5

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Leu  
 1 5 10 15

Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr  
 20 25 30

Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val  
 35 40 45

Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp  
 50 55 60

Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp  
 65 70 75 80

Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn  
 85 90 95

Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser  
 100 105 110

Ala Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn  
 115 120 125

Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe  
 130 135 140

Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly  
 145 150 155 160

Asp

<210> 6

<211> 858

<212> DNA

<213> Homo sapiens

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atgtccaatg ccaccctcggt cagctacatt gtgcagatcc tgagccgcta cgacatcgcc 180  
ctggtccagg aggtcagaga cagccacctg actgccgtgg ggaagctgct ggacaacctc 240  
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gtcaggttct tctcccggtt cacagaggc agggagtttgc ccattgttcc cctgcattgcg 480  
gcccccggggg acgcagttagc cgagatcgac gctctctatg acgtctaccc ggatgtccaa 540  
gagaaatggg gcttggagga cgtcatgttgc atgggcact tcaatgcggg ctgcagctat 600  
gtgagaccct cccagtggtc atccatccgc ctgtggacaa gccccaccc ttccagtg 660  
atccccgaca gcgcgtgacac cacagctaca cccacgcact gtgcctatga caggatcg 720  
gttgcaggga tgctgctccg agggccgtt gttcccgact cggctttcc cttaacttc 780  
caggctgcct atggcctgag tgaccaactg gcccaagcca tcagtgacca ctatccagtg 840  
gaggtgatgc tgaagtga 858

<210> 7

<211> 721

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG-1 light chain

<400> 7

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atccagatga cccagagccc aagcagcctg agcgccagcg tgggtgacag agtgaccatc 120  
acctgttaat ccagtcagag ctttttatat agtagcaatc aaaagatcta cttggcctgg 180  
taccagcaga agccaggtaa ggctccaaag ctgctgatct actgggcata cactaggaa 240  
tctggtgtgc caagcagatt cagcggtac ggttagcggta ccgacttcac cttcaccatc 300

agcagcctcc agccagagga catcgccacc tactactgcc agcaatatta tagatatcct	360
cggacgttcg gccaaggggac caaggtggaa atcaaacgaa ctgtggctgc accatctgtc	420
ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg	480
ctgaataact tctatcccag agaggccaaa gtacagtggaa aggtggataa cgccctccaa	540
tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc	600
agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgccctgcga	660
gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgttag	720
a	721

&lt;210&gt; 8

&lt;211&gt; 730

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG-1 light chain

<400> 8	
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cactccgaca tccagatgac ccagagccca agcagcctga gcccgcgt gggtgacaga	120
gtgaccatca cctgtaagtc cagtcagagc cttttatata gtagcaatca aaagatctac	180
ttggccttgtt accagcagaa gccaggtaag gctccaaagc tgctgatcta ctgggcattcc	240
actaggaaat ctggtgtgcc aagcagattc agcggtagcg gtagcggtac cgacttcacc	300
ttcaccatca gcagcctcca gccagaggac atcgccacct actactgcca gcaatattat	360
agatatcctc ggacgttcgg ccaaggggacc aaggtggaaa tcaaacgaac tgtggctgca	420
ccatctgtct tcattttccc gccatctgat gagcagttga aatctggAAC tgccctgtt	480
gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac	540
gccctccaat cggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc	600
tacagcctca gcagcaccct gacgctgagc aaagcagact acgagaaaca caaagtctac	660
gcctgcgaag tcacccatca gggcctgagc tcgcccgtca caaagagctt caacagggg	720
gagtgttaga	730

<210> 9

<211> 239

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG-1 light chain

<400> 9

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
1 5 10 15

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
20 25 30

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu  
35 40 45

Leu Tyr Ser Ser Asn Gln Lys Ile Tyr Leu Ala Trp Tyr Gln Gln Lys  
50 55 60

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu  
65 70 75 80

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe  
85 90 95

Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr  
100 105 110

Cys Gln Gln Tyr Tyr Arg Tyr Pro Arg Thr Phe Gly Gln Gly Thr Lys  
115 120 125

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro  
130 135 140

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu  
145 150 155 160

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp  
165 170 175

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp  
 180 185 190

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys  
 195 200 205

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln  
 210 215 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 225 230 235

<210> 10

<211> 1404

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG-1 heavy chain

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ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagataacaat	240	
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300	
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360	
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ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtccctc aggactctac	600	
tccctcagca gcgtggtgac cgtccctcc agcagcttgg gcacccagac ctacatctgc	660	
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720	
gaca <sup>144</sup> aaaactc acacatgccc accgtcccc gcacctgaac tcctgggggg accgtcagtc	780	
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tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac	900
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac	960
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag	1020
tgcaaggctc ccaacaaagc cctcccgacc cccatcgaga aaaccatctc caaagccaaa	1080
gggcagcccc gagaaccaca ggtgtacacc ctgccccat cccggatga gctgaccaag	1140
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gacggctcct ttttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg	1320
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ctctccctgt ctccggtaa atga	1404

<210> 11

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Hybrid hinge

<220>

<221> CDS

<222> (1)..(15)

<223>

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<210> 12

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Hybrid hinge

<400> 12

Asp Lys Thr His Thr  
1               5

<210> 13

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 13

ccgggtaaag ggagcggcgg gctgaagatc gcagcattca ac               42

<210> 14

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 14

gagagggaca gaggcccatt tccctcgccg cccgacttct ag               42

<210> 15

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 15

Leu Ser Leu Ser Pro Gly Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala  
1 5 10 15

Phe Asn

<210> 16

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 16

ccgaaaggga gcggcggttctt gaagatcgca gccttcaac 39

<210> 17

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 17

gagagggaca gaggcttcc ctcgccccc gacttctag 39

<210> 18

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 18

Leu Ser Leu Ser Pro Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe  
1                   5                   10                   15

Asn

<210> 19

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 19

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36

<210> 20

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 20

gagagggaca gaggcccctc gccgccccgac ttcttag

36

<210> 21

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 21

Leu Ser Leu Ser Pro Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn  
1 5 10 15

<210> 22

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 22

<210> 23

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 23

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<210> 24

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 24

Pro Pro Cys Pro Ala Pro Glu Gly Ser Gly Gly Leu Lys Ile Ala Ala  
1 5 10 15

Phe Asn

<210> 25

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 25

gcacacctgaag gcgggctgaa gatcgccagcc ttcaac

36

<210> 26

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 26

ggtggcacgg gtcgtggact tccgccccgac ttcttag

36

<210> 27

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 27

Pro Pro Cys Pro Ala Pro Glu Gly Gly Leu Lys Ile Ala Ala Phe Asn  
1 5 10 15

<210> 28

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 28

gagtgtccac cgtgtccagc accagagggg agcggcgccc tgaagatcg 57

<210> 29

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

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ctgtttttag ttttgtacgac acagactaca ggtggcacag gtcgtggct 57

<210> 30

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 30

Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro  
1 5 10 15

Glu Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe  
20 25

<210> 31

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 31

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<210> 32

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 32

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<210> 33

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 33

Asp	Lys	Thr	His	Thr	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro
1															15

Glu	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe
20								25

<210> 34

<211> 1554

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 34

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tgcaaggctt	ctggctacac	cttcagtgcc	tactggatag	agtgggtgcg	ccaggctcca	180
ggaaagggcc	tcgagtgggt	cggagagatt	ttacctggaa	gtaataattc	tagataacaat	240
gagaagttca	agggccgagt	gacagtca	agagacacat	ccacaaacac	agcctacatg	300
gagctcagca	gcctgaggtc	tgaggacaca	gccgtctatt	actgtgcaag	atcctacgac	360
tttgccttgtt	ttgcttactg	gggccaaggg	actctggtca	cagtctcctc	agcctccacc	420
aagggccat	cgtcttccc	cctggcaccc	tcctccaaga	gcacctctgg	gggcacagcg	480
gccctggct	gcctggcaa	ggactacttc	cccgaaccgg	tgacggtgtc	gtggaactca	540
ggcgccctga	ccagcggcgt	gcacaccc	ccggctgtcc	tacagtcc	aggactctac	600
tccctcagca	gcgtggtgac	cgtgccctcc	agcagcttg	gcacccagac	ctacatctgc	660
aacgtgaatc	acaagcccag	caacaccaag	gtggacaaga	aagttgagcc	caaatcttgt	720

gacaaaactc acacatgccc accgtgccca gcacctgaag ggagcggcgg gctgaagatc	780
gcagccttca acatccagac atttggggag accaagatgt ccaatgccac cctcgtcagc	840
tacattgtgc agatcctgag ccgctacgac atcgccctgg tccaggaggt cagagacagc	900
cacctgactg ccgtggggaa gctgctggac aacctaatac aggacgcacc agacacatat	960
cactacgtgg tcagttagcc actgggacgg aacagctata aggacgcta cctgttcgtg	1020
tacaggcctg accaggtgtc tgcgggtggac agctactact acgatgatgg ctgcgagccc	1080
tgcgggaacg acaccttcaa ccgagagcca gccattgtca gtttcttctc ccggttcaca	1140
gaggtcaggg agtttgcatt tttcccttg catgcggccc cggggacgc agtagccag	1200
atcgacgctc tctatgacgt ctacctggat gtccaagaga aatggggctt ggaggacgtc	1260
atgttcatgg gcgacttcaa tgcggctgc agctatgtga gaccctccca gtggtcatcc	1320
atccgcctgt ggacaagccc cacctccag tggctgatcc ccgacagcgc tgacaccaca	1380
gctacaccca cgcaactgtgc ctatgacagg atcgtggttg cagggatgct gctccgaggg	1440
gccgttgttc ccgactcggc tttcccttt aacttccagg ctgcctatgg cctgagtgac	1500
caactggccc aagccatcag tgaccactat ccagtggagg tgatgctgaa gtga	1554

<210> 35

<211> 1554

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 35	
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tgcaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagataaat	240
gagaagttca agggccgagt gacagtcaat agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggc tgaggacaca gccgtctatt acttgcaag atcctacgac	360
tttgccttgt ttgcttactg gggccaagg actctggta cagtcctc cgcctccacc	420
aagggccat cggcttcccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480

gccctgggct	gcctggtcaa	ggactacttc	cccgaaccgg	tgacggtgtc	gtgaaactca	540
ggcgccctga	ccagcggcgt	gcacaccttc	ccggctgtcc	tacagtccctc	aggactctac	600
tccctcagca	gcgtggtgac	cgtgccctcc	agcagcttgg	gcacccagac	ctacatctgc	660
aacgtgaatc	acaagcccag	caacaccaag	gtggacaaga	aagttgagcc	caaatcttgt	720
gacaaaactc	acacatgtcc	accgtgtcca	gcaccagagg	ggagcggcgg	gctgaagatc	780
gcagccttca	acatccagac	atttggggag	accaagatgt	ccaatgccac	cctcgtagc	840
tacattgtgc	agatcctgag	ccgctacgac	atcgccctgg	tccaggaggt	cagagacagc	900
cacctgactg	ccgtggggaa	gctgctggac	aacctaatac	aggacgcacc	agacacctat	960
cactacgtgg	tcaagtggcc	actgggacgg	aacagctata	aggagcgcta	cctgttcgtg	1020
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tgcgggaacg	acaccttcaa	ccgagagcca	gccattgtca	ggttttctc	ccggttcaca	1140
gaggtcaggg	agtttgcacat	tgttccccctg	catgcggccc	cggggacgc	agttagccgag	1200
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gctacaccca	cgcactgtgc	ctatgacagg	atcgtggttg	cagggatgct	gctccgaggg	1440
gccggttttc	ccgactcggc	tcttcccttt	aacttccagg	ctgcctatgg	cctgagtgac	1500
caactggccc	aagccatcag	tgaccactat	ccagtggagg	tgtatgtgaa	gtga	1554

<210> 36

<211> 1563

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 36

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aagggtcct	gcaaggcttc	tggctacacc	ttcagtgcct	actggataga	gtgggtgcgc	180

caggctccag	gaaaggcct	cgagtggtc	ggagagattt	tacctggaag	taataattct	240
agataacaatg	agaagttcaa	gggccgagtg	acagtcacta	gagacacatc	cacaaacaca	300
gcctacatgg	agctcagcag	cctgaggtct	gaggacacag	ccgtctatta	cttgcaaga	360
tcctacgact	ttgcctggtt	tgcttactgg	ggccaaggga	ctctggtcac	agtctcctca	420
gcctccacca	agggcccattc	ggtcttcccc	ctggcaccct	cctccaagag	cacctctggg	480
ggcacagcgg	ccctgggctg	cctggtcaag	gactacttcc	ccgaaccgg	gacggtgtcg	540
tggaactcag	gcgcctgac	cagcggcgtg	cacaccttcc	cggctgtcct	acagtccctca	600
ggactctact	ccctcagcag	cgtggtgacc	gtgccctcca	gcagcttggg	cacccagacc	660
tacatctgca	acgtgaatca	caagcccagc	aacaccaagg	tggacaagaa	agttgagccc	720
aaatcttgtg	acaaaaactca	cacatgtcca	ccgtgtccag	caccagaggg	gagcggcggg	780
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gacacctatc	actacgttgt	cagttagcca	ctgggacgga	acagctataa	ggagcgctac	1020
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gtagccgaga	tcgacgctct	ctatgacgtc	tacctggatg	tccaaagagaa	atggggcttg	1260
gaggacgtca	tgttgatggg	cgacttcaat	gcgggctgca	gctatgtgag	accctcccag	1320
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gacaccacag	ctacacccac	gcactgtgcc	tatgacagga	tcgtggttgc	aggatgctg	1440
ctccgagggg	ccgttgttcc	cgactcggct	cttcccttta	acttccaggc	tgcctatggc	1500
ctgagtgacc	aactggccca	agccatcaat	gaccactatc	cagtggaggt	gatgctgaag	1560
tga						1563

&lt;210&gt; 37

&lt;211&gt; 1554

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<220>

<221> CDS

<222> (1)..(1554)

<223>

<400> 37

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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1           5                   10                  15

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48

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag		
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys		
20	25	30

96

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc  
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45

144

agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc  
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60

192

240

gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac  
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn  
85 90 95

288

336

384

caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg  
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
130 135 140

432

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg  
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 145 150 155 160

480

tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 180	185	190	576
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 195	200	205	624
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 210	215	220	672
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 225	230	235	720
gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ggg agc ggc Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Gly Ser Gly 245	250	255	768
ggg ctg aag atc gca gcc ttc aac atc cag aca ttt ggg gag acc aag Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys 260	265	270	816
atg tcc aat gcc acc ctc gtc agc tac att gtg cag atc ctg agc cgc Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg 275	280	285	864
tac gac atc gcc ctg gtc cag gag gtc aga gac agc cac ctg act gcc Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala 290	295	300	912
gtg ggg aag ctg ctg gac aac ctc aat cag gag gca cca gac acc tat Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr 305	310	315	960
cac tac gtg gtc agt gag cca ctg gga cgg aac agc tat aag gag cgc His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg 325	330	335	1008
tac ctg ttc gtg tac agg cct gac cag gtg tct gcg gtg gac agc tac Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr 340	345	350	1056
tac tac gat gat ggc tgc gag ccc tgc ggg aac gac acc ttc aac cga Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg 355	360	365	1104
gag cca gcc att gtc agg ttc ttc tcc cgg ttc aca gag gtc agg gag Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu 370	375	380	1152
ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg gac gca gta gcc gag Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu 385	390	395	1200
atc gac gct ctc tat gac gtc tac ctg gat gtc caa gag aaa tgg ggc Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly 405	410	415	1248

ttg gag gac gtc atg ttg atg ggc gac ttc aat gcg ggc tgc agc tat		1296	
Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr			
420	425	430	
gtg aga ccc tcc cag tgg tca tcc atc cgc ctg tgg aca agc ccc acc		1344	
Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr			
435	440	445	
ttc cag tgg ctg atc ccc gac agc gct gac acc aca gct aca ccc acg		1392	
Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr			
450	455	460	
cac tgt gcc tat gac agg atc gtg gtt gca ggg atg ctg ctc cga ggg		1440	
His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly			
465	470	475	480
gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac ttc cag gct gcc tat		1488	
Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr			
485	490	495	
ggc ctg agt gac caa ctg gcc caa gcc atc agt gac cac tat cca gtg		1536	
Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val			
500	505	510	
gag gtg atg ctg aag tga		1554	
Glu Val Met Leu Lys			
515			

<210> 38  
<211> 517  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Humanised HMFG1 Fd - DNase I fusion  
<400> 38  
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
1 5 10 15  
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
20 25 30  
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45  
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu

50	55	60
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn		
65	70	75
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn		
85	90	95
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val		
100	105	110
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly		
115	120	125
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser		
130	135	140
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala		
145	150	155
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val		
165	170	175
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala		
180	185	190
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val		
195	200	205
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His		
210	215	220
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys		
225	230	235
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Gly Ser Gly		
245	250	255
Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys		
260	265	270
Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg		
275	280	285

Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala  
 290                           295                           300

Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr  
 305                           310                           315                           320

His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg  
 325                           330                           335

Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr  
 340                           345                           350

Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg  
 355                           360                           365

Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu  
 370                           375                           380

Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu  
 385                           390                           395                           400

Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly  
 405                           410                           415

Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr  
 420                           425                           430

Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr  
 435                           440                           445

Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr  
 450                           455                           460

His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly  
 465                           470                           475                           480

Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr  
 485                           490                           495

Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val  
 500                           505                           510

Glu Val Met Leu Lys  
 515

<210> 39  
 <211> 1584  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 39	
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tgcaggctt ctggctacac cttcagtgcc tactggatag	180
agtgggtgcg ccaggctcca	
ggaaagggcc tcgagtgggt cgagagatt ttacctggaa	240
gtaataattc tagatacaat	
gagaagttca agggccgagt gacagtca	300
agagacacat ccacaaacac agcctacatg	
gagctcagca gcctgaggc tgaggacaca	360
gccgtctatt actgtgcaag atcctacgac	
tttgcctggc ttgcttactg gggccaaggg	420
actctggtca cagtctcctc agcctccacc	
aagggccat cggcttccc cctggcaccc	480
tcctccaaga gcacctctgg gggcacagcg	
gccctggct gcctggcaa ggactacttc	540
cccgaaccgg tgacgggtgc gtggaactca	
ggcgccctga ccagcggcgt gcacaccc	600
ccggctgtcc tacagtctc aggactctac	
tccctcagca gcgtggtgac cgtgcctcc	660
agcagcttgg gcacccagac ctacatctgc	
aacgtgaatc acaagcccag caacaccaag	720
gtggacaaga aagttgagcc caaatcttgt	
gacaaaactc acacatgtcc accgtgtcca	780
gcaccagagg ggagcggcgg gctgaagatc	
gcagcctca acatccagac atttggggag	840
accaagatgt ccaatgccac cctcgctcagc	
tacatttgtc agatcctgag ccgctacgac	900
atcgccctgg tccaggaggt cagagacagc	
cacctgactg ccgtgggaa gctgctggac	960
aacctcaatc aggacgcacc agacacctat	
cactacgtgg tcaagtggcc actgggacgg	1020
aacagctata aggagcgcta cctgttcgtg	
tacaggcctg accaggtgtc tgcgggtggac	1080
agctactact acgatgatgg ctgcgagccc	
tgcgggaacg acaccttcaa ccgagagcca	1140
gccattgtca gttttttctc ccgggttcaca	
gaggtcaggg agtttgcacat tggccat	1200
tgttccctcg catgcggccc cggggacgc	
agtagccgag atcgacgctc tctatgacgt	1260
ctacctggat gtccaaagaga aatggggctt	
ggaggacgtc atgttgcatgg gcgacttcaa	1320
tgcgggtgc agctatgtga gaccctccca	
gtggtcatcc	

atccgcctgt ggacaaggccc caccttccag tggctgatcc ccgacagcgc tgacaccaca 1380  
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 gccgttggc ccgactcggc tcttccttt aacttccagg ctgcctatgg cctgagtgac 1500  
 caactggccc aagccatcag tgaccactat ccagtggagg tcatgctgaa gggggcgga 1560  
 cccaaaaaga agcgcaaggt ttga 1584

<210> 40

<211> 1584

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

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 tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca 180  
 gaaaaagggcc tcgagtggtt cgagagatt ttacctggaa gtaataattc tagataaat 240  
 gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg 300  
 gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac 360  
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 aagggccat cggcttcccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 480  
 gccctggct gcctggtcaa ggactacttc cccgaaccgg tgacgggtgc gtggaaactca 540  
 ggcgcctga ccagcggcgt gcacaccccttc ccggctgtcc tacagtcctc aggactctac 600  
 tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 660  
 aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 720  
 gacaaaactc acacatgtcc accgtgtcca gcaccagagg ggagcggcgg gctgaagatc 780  
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 atcgacgctc tctatgacgt ctacctggat gtccaaagaga aatggggctt ggaggacgtc 1260  
 atgttcatgg gcgacttcaa tgcgggctgc agctatgtga gaccctccca gtggtcatcc 1320  
 atccgcctgt ggacaagccc caccttccag tggctgatcc ccgacagcgc tgacaccaca 1380  
 gctacaccca cgcaactgtgc ctatgacagg atcgtggttg cagggatgct gctccgaggg 1440  
 gccgttggc ccgactcggc tcttcccttt aacttccagg ctgcctatgg cctgagtgac 1500  
 caactggccc aagccatcag tgaccactat ccagtgagg tgatgctgaa ggggggcgga 1560  
 cccaaaaaga agcgcaaggt ttga 1584

&lt;210&gt; 41

&lt;211&gt; 1593

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

<400> 41  
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 cactcccagg tgcagctggc gcagtctggc gcagaggtga aaaagcctgg ggcctcagtg 120  
 aaggtgtcct gcaaggcttc tggctacacc ttcagtgcct actggataga gtgggtgcgc 180  
 caggctccag gaaaggcct cgagtggcgc ggagagattt tacctggaag taataattct 240  
 agataacaatg agaagttcaa gggccgagtg acagtcacta gagacacatc cacaacaca 300  
 gcctacatgg agctcagcag cctgaggtct gaggacacag ccgtctatta ctgtgcaaga 360  
 tcctacgact ttgcctggtt tgcttactgg ggccaaggga ctctggcac agtctcctca 420  
 gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480  
 ggcacagcgg ccctggcgtg cctggtaag gactactcc ccgaaccggc gacgggtgtcg 540  
 tggaaactcag ggcgcctgac cagcggcgtg cacacccctcc cggctgtcct acagtccctca 600  
 ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 660

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	720
aaatcttgtg acaaaaactca cacatgtcca ccgtgtccag caccagaggg gagcggcg	780
ctgaagatcg cagccttcaa catccagaca tttggggaga ccaagatgtc caatgccacc	840
ctcgtcagct acatttgca gatcctgagc cgctacgaca tcgcccgtt ccaggaggc	900
agagacagcc acctgactgc cgtggggaa ctgctggaca acctaatac ggacgcacca	960
gacacctatac actacgttgt cagttagcca ctgggacgga acagctataa ggagcgctac	1020
ctgttcgtgt acaggcctga ccaggtgtct gcgggtggaca gctactacta cgatgtatgc	1080
tgcgagccct gcgggaacga caccttcaac cgagagccag ccattgtcag gttttctcc	1140
cgttcacag aggtcaggga gtttgcatt gttccctgc atgcggcccc gggggacgca	1200
gtagccgaga tcgacgctct ctatgacgtc tacctggatg tccaaagagaa atggggcttg	1260
gaggacgtca tggtgatggg cgacttcaat gcgggctgca gctatgtgag accctccag	1320
tggtcatcca tccgcctgtg gacaagcccc accttccagt ggctgatccc cgacagcgct	1380
gacaccacag ctacacccac gcactgtgcc tatgacagga tcgtgggtgc agggatgctg	1440
ctccgagggg cgttgttcc cgactcggtcttta acttccaggc tgcctatggc	1500
ctgagtgacc aactggccca agccatcagt gaccactatac cagtggaggt gatgctgaag	1560
gggggcggac ccaaaaagaa gcgcaagggt tga	1593

<210> 42

<211> 1584

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<220>

<221> CDS

<222> (1)..(1584)

<223>

<400> 42

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly 1 5 10 15	48
gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys 20 25 30	96
cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe 35 40 45	144
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu 50 55 60	192
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn 65 70 75 80	240
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn 85 90 95	288
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val 100 105 110	336
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly 115 120 125	384
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser 130 135 140	432
gtc ttc ccc ctg gca ccc tcc aag agc acc tct ggg ggc aca gcg Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala 145 150 155 160	480
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val 165 170 175	528
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 180 185 190	576
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc acc Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 195 200 205	624
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 210 215 220	672
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 225 230 235 240	720

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ggg agc ggc Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Gly Ser Gly 245 250 255	768
ggg ctg aag atc gca gcc ttc aac atc cag aca ttt ggg gag acc aag Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys 260 265 270	816
atg tcc aat gcc acc ctc gtc agc tac att gtg cag atc ctg agc cgc Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg 275 280 285	864
tac gac atc gcc ctg gtc cag gag gtc aga gac agc cac ctg act gcc Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala 290 295 300	912
gtg ggg aag ctg ctg gac aac ctc aat cag gac gca cca gac acc tat Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr 305 310 315 320	960
cac tac gtg gtc agt gag cca ctg gga cgg aac agc tat aag gag cgc His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg 325 330 335	1008
tac ctg ttc gtg tac agg cct gac cag gtg tct gcg gtg gac agc tac Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr 340 345 350	1056
tac tac gat gat ggc tgc gag ccc tgc ggg aac gac acc ttc aac cga Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg 355 360 365	1104
gag cca gcc att gtc agg ttc ttc tcc cgg ttc aca gag gtc agg gag Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu 370 375 380	1152
ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg gac gca gta gcc gag Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu 385 390 395 400	1200
atc gac gct ctc tat gac gtc tac ctg gat gtc caa gag aaa tgg ggc Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly 405 410 415	1248
ttg gag gac gtc atg ttg atg ggc gac ttc aat gcg ggc tgc agc tat Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr 420 425 430	1296
gtg aga ccc tcc cag tgg tca tcc atc cgc ctg tgg aca agc ccc acc Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr 435 440 445	1344
ttc cag tgg ctg atc ccc gac agc gct gac acc aca gct aca ccc acg Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr 450 455 460	1392
cac tgt gcc tat gac agg atc gtg gtt gca ggg atg ctg ctc cga ggg His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly	1440

465	470	475	480	
gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac ttc cag gct gcc tat Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr 485 490 495				1488
ggc ctg agt gac caa ctg gcc caa gcc atc agt gac cac tat cca gtg Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val 500 505 510				1536
gag gtg atg ctg aag ggg ggc gga ccc aaa aag aag cgc aag gtt tga Glu Val Met Leu Lys Gly Gly Pro Lys Lys Lys Arg Lys Val 515 520 525				1584
<210> 43				
<211> 527				
<212> PRT				
<213> Artificial Sequence				
<220>				
<223> Humanised HMFG1 Fd - DNase I fusion				
<400> 43				
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly 1 5 10 15				
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys 20 25 30				
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe 35 40 45				
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu 50 55 60				
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn 65 70 75 80				
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn 85 90 95				
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val 100 105 110				

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Gly Ser Gly  
245 250 255

Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys  
260 265 270

Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg  
275 280 285

Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala  
290 295 300

His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg  
325 330 335

Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr  
340 345 350

Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu  
370 375 380

Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu  
385 390 395 400

Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly  
405 410 415

Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr  
420 425 430

Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr  
435 440 445

Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr  
450 455 460

His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly  
465 470 475 480

Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr  
485 490 495

Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val  
500 505 510

Glu Val Met Leu Lys Gly Gly Gly Pro Lys Lys Lys Arg Lys Val  
515 520 525

<210> 44

<211> 2196

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 44  
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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca 180  
ggaaagggcc tcgagtggtt cgagagatt ttacctggaa gtaataattc tagataacaat 240  
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg 300  
gagctcagca gcctgaggtc tgaggacaca gccgtctatt acttgcaag atcctacgac 360  
ttgccttgtt ttgcttactg gggccaaggg actctggtca cagtctcctc agcctccacc 420  
aagggccat cggcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 480  
gccctggct gcctggtcaa ggactacttc cccgaaccgg tgacgggtgc gtggaaactca 540  
ggcgccctga ccagcggcgt gcacacccctc ccggctgtcc tacagtccctc aggactctac 600  
tccctcagca gcgtggtgac cgtccctcc agcagcttgg gcacccagac ctacatctgc 660  
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 720  
gacaaaactc acacatgccc accgtgcccga gcacctgaac tcctgggggg accgtcagtc 780  
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 840  
tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 900  
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 960  
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 1020  
tgcaaggctt ccaacaaagc cttccagcc cccatcgaga aaaccatctc caaagccaaa 1080  
ggcagcccc gagaaccaca ggtgtacacc ctgccccat cccggatga gctgaccaag 1140  
aaccaggta cctgacccctg cctggtaaa ggcttctatc ccagcgacat cgccgtggag 1200  
tgggagagca atggcagcc ggagaacaac tacaagacca cgcctccgt gctggactcc 1260  
gacggctcct tttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1320  
aacgtttctt catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1380  
ctctccctgt ctccggtaa agggagcggc gggctgaaga tcgcagcctt caacatccag 1440  
acatttgggg agaccaagat gtccaatgcc accctcgta gctacattgt gcagatcctg 1500  
agccgctacg acatcgccct ggtccaggag gtcagagaca gccacctgac tgccgtgggg 1560  
aagctgctgg acaacctcaa tcaggacgca ccagacacct atcactacgt ggtcagtgag 1620  
ccactgggac ggaacagcta taaggagcgc tacctgttcg tgtacaggcc tgaccaggtg 1680  
tctgcggtgg acagctacta ctacgatgtat ggctgctgagc cctgcggaa cgacaccc 1740

aaccgagagc cagccattgt caggttcttc tcccggttca cagaggtcag ggagttgcc 1800  
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gtctacctgg atgtccaaga gaaatggggc ttggaggacg tcataatgtat gggcgacttc 1920  
aatgcgggct gcagctatgt gagaccctcc cagtggtcat ccatccgcct gtggacaagc 1980  
cccaccttcc agtggctgat ccccgacagc gctgacacca cagctacacc cacgcactgt 2040  
gcctatgaca ggatcgttgt tgcaaggatg ctgctccgag gggccgttgt tcccgactcg 2100  
gctctccct ttaacttcca ggctgcctat ggcctgagtg accaactggc ccaagccatc 2160  
agtgaccact atccagtgga ggtgatgctg aagtga 2196

<210> 45

<211> 2196

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<220>

<221> CDS

<222> (1)..(2196)

<223>

<400> 45

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt  
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
1 5 10 15

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag 96  
 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 20 25 30

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc 144  
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 . 40 . 45

agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc 192  
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60

gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat 240

Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn	
65				70					75				80			
gag	aag	tac	aag	ggc	cga	gtg	aca	gtc	act	aga	gac	aca	tcc	aca	aac	288
Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn	
	85								90				95			
aca	gcc	tac	atg	gag	ctc	agc	agc	ctg	agg	tct	gag	gac	aca	gcc	gtc	336
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
	100								105				110			
tat	tac	tgt	gca	aga	tcc	tac	gac	ttt	gcc	tgg	ttt	gct	tac	tgg	ggc	384
Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly	
	115							120				125				
caa	ggg	act	ctg	gtc	aca	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	432
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	
	130							135				140				
gtc	tcc	ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	480
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	
	145							150				155			160	
gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	528
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	
	165							170				175				
tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	576
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	
	180							185				190				
gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	624
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
	195							200				205				
ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	672
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	
	210							215				220				
aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt	720
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	
	225							230				235			240	
gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	ctc	ctg	ggg	768
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	
	245							250				255				
gga	ccg	tca	gtc	tcc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	816
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	
	260							265				270				
atc	tcc	cg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	864
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	
	275							280				285				
gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	912
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	
	290							295				300				

cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr 305 310 315 320	960
cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 325 330 335	1008
aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile 340 345 350	1056
gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 355 360 365	1104
tac acc ctg ccc cca tcc cggt gat gag ctg acc aag aac cag gtc agc Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser 370 375 380	1152
ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 385 390 395 400	1200
tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro 405 410 415	1248
gtg ctg gac tcc gac ggc tcc ttc ctc tac agc aag ctc acc gtg Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val 420 425 430	1296
gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met 435 440 445	1344
cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 450 455 460	1392
ccg ggt aaa ggg agc ggc ggg ctg aag atc gca gcc ttc aac atc cag Pro Gly Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln 465 470 475 480	1440
aca ttt ggg gag acc aag atg tcc aat gcc acc ctc gtc agc tac att Thr Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile 485 490 495	1488
gtg cag atc ctg agc cgc tac gac atc gcc ctg gtc cag gag gtc aga Val Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg 500 505 510	1536
gac agc cac ctg act gcc gtg ggg aag ctg ctg gac aac ctc aat cag Asp Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln 515 520 525	1584
gac gca cca gac acc tat cac tac gtg gtc agt gag cca ctg gga cgg Asp Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg 530 535 540	1632

aac agc tat aag gag cgc tac ctg ttc gtg tac agg cct gac cag gtg Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val 545 550 555 560	1680
tct gcg gtg gac agc tac tac tac gat gat ggc tgc gag ccc tgc ggg Ser Ala Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly 565 570 575	1728
aac gac acc ttc aac cga gag cca gcc att gtc agg ttc ttc tcc cgg Asn Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg 580 585 590	1776
ttc aca gag gtc agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg Phe Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro 595 600 605	1824
ggg gac gca gta gcc gag atc gac gct ctc tat gac gtc tac ctg gat Gly Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp 610 615 620	1872
gtc caa gag aaa tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc Val Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe 625 630 635 640	1920
aat gcg ggc tgc agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg 645 650 655	1968
ctg tgg aca agc ccc acc ttc cag tgg ctg atc ccc gac agc gct gac Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp 660 665 670	2016
acc aca gct aca ccc acg cac tgt gcc tat gac agg atc gtg gtt gca Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala 675 680 685	2064
ggg atg ctg ctc cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt Gly Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe 690 695 700	2112
aac ttc cag gct gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc Asn Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile 705 710 715 720	2160
agt gac cac tat cca gtg gag gtg atg ctg aag tga Ser Asp His Tyr Pro Val Glu Val Met Leu Lys 725 730	2196

&lt;210&gt; 46

&lt;211&gt; 731

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 heavy chain - DNase I fusion

&lt;400&gt; 46

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1															15

Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
															30
20								25							

Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
															45
35							40								

Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
															60
50					55										

Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn
															80
65					70				75						

Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn
															95
85								90							

Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val
															110
100								105							

Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly
															125
115						120									

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
															140
130							135								

Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala
															160
145					150				155						

Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
															175
165								170							

Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
															190
180								185							

Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
															205
195								200							

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 355 360 365

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
 370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
 420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 450 455 460

Pro Gly Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln  
 465 470 475 480

Thr Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile  
 485 490 495

Val Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg  
 500 505 510

Asp Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln  
 515 520 525

Asp Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg  
 530 535 540

Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val  
 545 550 555 560

Ser Ala Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly  
 565 570 575

Asn Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg  
 580 585 590

Phe Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro  
 595 600 605

Gly Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp  
 610 615 620

Val Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe  
 625 630 635 640

Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg  
 645 650 655

Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp  
 660 665 670

Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala

675

680

685

Gly Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe  
 690 695 700

Asn Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile  
 705 710 715 720

Ser Asp His Tyr Pro Val Glu Val Met Leu Lys  
 725 730

&lt;210&gt; 47

&lt;211&gt; 2193

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 heavy chain - DNase I fusion

&lt;400&gt; 47

atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt ccactcccg 60

gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg gggcctcagt gaagggtgtcc 120

tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca 180

ggaaagggcc tcgagtggtt cgagagagatt ttacctggaa gtaataattc tagataacaat 240

gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg 300

gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac 360

tttgccttgtt ttgcttactg gggccaaggg actctggta cagtctcctc agcctccacc 420

aagggcccatt cggctttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 480

gccctggct gcctggtaa ggactacttc cccgaaccgg tgacgggtgc gtggaactca 540

ggcgccctga ccagcggcgt gcacaccccttc ccggctgtcc tacagtctc aggactctac 600

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 660

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 720

gacaaaactc acacatgccc accgtgccca gcacccctgaac tcctgggggg accgtcagtc 780

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 840

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 900

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac	960
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag	1020
tgcaaggctc ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaa	1080
ggcagcccc gagaaccaca ggtgtacacc ctgccccat cccggatga gctgaccaag	1140
aaccaggta gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag	1200
tggagagca atggcagcc ggagaacaac tacaagacca cgcctccgt gctggactcc	1260
gacggctcct ttttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg	1320
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc	1380
ctctccctgt ctccgaaggg gagcggcggg ctgaagatcg cagcattcaa catccagaca	1440
tttgggaga ccaagatgtc caatgccacc ctcgtcagct acatttgca gatcctgagc	1500
cgctacgaca tcgcccgtt ccaggaggc agagacagcc acctgactgc cgtggggaa	1560
ctgctggaca acctcaatca ggacgcacca gacacctatc actacgtggt cagttagcca	1620
ctgggacgga acagctataa ggagcgctac ctgttcgtgt acaggcctga ccaggtgtct	1680
gcgggtggaca gctactacta cgatgatggc tgcgagccct gcgggaacga caccattcaac	1740
cgagagccag ccattgtcag gttttctcc cggttcacag aggtcaggga gtttgccatt	1800
gttccctgc atgcggcccc gggggacgca gtagccgaga tcgacgctct ctatgacgtc	1860
tacctggatg tccaagagaa atggggcttg gaggacgtca tgttgatggg cgacttcaat	1920
gcgggctgca gctatgtgag accctccctag tggtcatcca tccgcctgtg gacaagcccc	1980
accttccagt ggctgatccc cgacagcgct gacaccacag ctacacccac gcactgtgcc	2040
tatgacagga tcgtgggtgc agggatgctg ctccgagggg ccgttggcc cgactcggct	2100
cttcccttta acttccaggc tgcctatggc ctgagtgacc aactggccca agccatcagt	2160
gaccactatc cagtggaggt gatgctgaag tga	2193

<210> 48

<211> 2193

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(2193)

&lt;223&gt;

<400>	48		
atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt			48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly			
1 5 10 15			
gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag			96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys			
20 25 30			
cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc			144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe			
35 40 45			
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc			192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu			
50 55 60			
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat			240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn			
65 70 75 80			
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac			288
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn			
85 90 95			
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc			336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val			
100 105 110			
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc			384
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly			
115 120 125			
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg			432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser			
130 135 140			
gtc ttc ccc ctg gca ccc tcc aag agc acc tct ggg ggc aca gcg			480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala			
145 150 155 160			
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg			528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val			
165 170 175			
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct			576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala			
180 185 190			

gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc acc gtg			624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val			
195	200	205	
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac			672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His			
210	215	220	
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt			720
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys			
225	230	235	240
gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg			768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly			
245	250	255	
gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg			816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met			
260	265	270	
atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac			864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His			
275	280	285	
gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg			912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val			
290	295	300	
cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac			960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr			
305	310	315	320
cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc			1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly			
325	330	335	
aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc			1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile			
340	345	350	
gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg			1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val			
355	360	365	
tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc			1152
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser			
370	375	380	
ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag			1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu			
385	390	395	400
tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc			1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro			
405	410	415	
gtg ctg gac tcc gac ggc tcc ttc ctc tac agc aag ctc acc acc gtg			1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val			

420	425	430	
gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met 435	440	445	1344
cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 450	455	460	1392
ccg aag ggg agc ggc ggg ctg aag atc gca gcc ttc aac atc cag aca Pro Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr 465	470	475	1440
ttt ggg gag acc aag atg tcc aat gcc acc ctc gtc agc tac att gtg Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val 485	490	495	1488
cag atc ctg agc cgc tac gac atc gcc ctg gtc cag gag gtc aga gac Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp 500	505	510	1536
agc cac ctg act gcc gtg ggg aag ctg ctg gac aac ctc aat cag gac Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp 515	520	525	1584
gca cca gac acc tat cac tac gtg gtc agt gag cca ctg gga cgg aac Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn 530	535	540	1632
agc tat aag gag cgc tac ctg ttc gtg tac agg cct gac cag gtg tct Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser 545	550	555	1680
gcg gtg gac agc tac tac tac gat gat ggc tgc gag ccc tgc ggg aac Ala Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn 565	570	575	1728
gac acc ttc aac cga gag cca gcc att gtc agg ttc ttc tcc cgg ttc Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe 580	585	590	1776
aca gag gtc agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly 595	600	605	1824
gac gca gta gcc gag atc gac gct ctc tat gac gtc tac ctg gat gtc Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val 610	615	620	1872
caa gag aaa tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc aat Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn 625	630	635	1920
gcg ggc tgc agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc ctg Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu 645	650	655	1968
tgg aca agc ccc acc ttc cag tgg ctg atc ccc gac agc gct gac acc			2016

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Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr
660 665 670

aca gct aca ccc acg cac tgt gcc tat gac agg atc gtg gtt gca ggg 2064
Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly
675 680 685

atg ctg ctc cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac 2112
Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn
690 695 700

ttc cag gct gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc agt 2160
Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser
705 710 715 720

gac cac tat cca gtg gag gtg atg ctg aag tga 2193
Asp His Tyr Pro Val Glu Val Met Leu Lys
725 730

<210> 49

<211> 730

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 49

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn
65 70 75 80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn
85 90 95

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Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
 115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165 170 . 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 355 360 365

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
 370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
 420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 450 455 460

Pro Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr  
 465 470 475 480

Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val  
 485 490 495

Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp  
 500 505 510

Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp  
 515 520 525

Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn  
 530 535 540

Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser  
 545 550 555 560

Ala Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn

565

570

575

Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe  
 580 585 590

Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly  
 595 600 605

Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val  
 610 615 620

Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn  
 625 630 635 640

Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu  
 645 650 655

Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr  
 660 665 670

Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly  
 675 680 685

Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn  
 690 695 700

Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser  
 705 710 715 720

Asp His Tyr Pro Val Glu Val Met Leu Lys  
 725 730

<210> 50

<211> 2190

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 50

atgggatgga gctgttatcat cctcttcttg gtagcaacag ctacaggtgt ccactcccaag

60

gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg gggcctcagt gaagggtgtcc	120
tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtggtt cgagagatt ttacctggaa gtaataattc tagatacat	240
gagaagttca agggccgagt gacagtcaact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgccttgtt ttgcttactg gggccaagg actctggtca cagtcctc ctc agcctccacc	420
aagggccat cggcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480
gccctggct gcctggtcaa ggactacttc cccgaaccgg tgacgggtgc gtggactca	540
ggcgccctga ccagcggcgt gcacaccccttc ccggctgtcc tacagtcctc aggactctac	600
tccctcagca gcgtggtgac cgtccctcc agcagcttgg gcacccagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720
gacaaaactc acacatgccc accgtgccca gcacctgaac tcctgggggg accgtcagtc	780
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	840
tgcgtgggg tggacgtgag ccacgaagac cctgagggtca agttcaactg gtacgtggac	900
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac	960
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag	1020
tgcaaggctt ccaacaaagc cttccagcc cccatcgaga aaaccatctc caaagccaaa	1080
ggcagcccc gagaaccaca ggtgtacacc ctgccccat cccggatga gctgaccaag	1140
aaccaggta gcctgacccctg cttggtaaaa ggcttctatc ccagcgacat cgccgtggag	1200
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctccgt gctggactcc	1260
gacggctcct tttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg	1320
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc	1380
ctctccctgt ccccgggag cggcgggctg aagatcgac cttcaacat ccagacattt	1440
ggggagacca agatgtccaa tgccaccctc gtcagctaca ttgtgcagat cctgagccgc	1500
tacgacatcg ccctggtcca ggaggtcaga gacagccacc tgactgccgt gggaaagctg	1560
ctggacaacc tcaatcagga cgcaccagac acctatcact acgtggtcag tgagccactg	1620
ggacggaaca gctataagga gcgctacctg ttcgtgtaca ggcctgacca ggtgtctgcg	1680
gtggacagct actactacga tcatggctgc gagccctgcg ggaacgacac cttcaaccga	1740
gagccagcca ttgtcagggtt cttctccgg ttcacagagg tcagggagtt tgccattgtt	1800

cccctgcatg cggccccggg ggacgcagta gccgagatcg acgctctcta tgacgtctac 1860  
 ctggatgtcc aagagaaatg gggcttggag gacgtcatgt tcatggcga cttcaatgcg 1920  
 ggctgcagct atgtgagacc ctcccagtgg tcatccatcc gcctgtggac aagccccacc 1980  
 ttccagtgcc tgatccccga cagcgctgac accacagcta caccacgca ctgtgcctat 2040  
 gacaggatcg tggttgcagg gatgctgctc cgaggggccg ttgttcccga ctccggcttt 2100  
 ccctttaact tccaggctgc ctatggcctg agtgaccaac tggcccaagc catcagtgac 2160  
 cactatccag tggaggtgat gctgaagtga 2190

<210> 51

<211> 2190

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<220>

<221> CDS

<222> (1)..(2190)

<223>

<400> 51

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt	48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag	96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35 40 45	

agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc	192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
50 55 60	

gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat	240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn	
65 70 75 80	

gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn 85 90 95	288
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val 100 105 110	336
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly 115 120 125	384
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser 130 135 140	432
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala 145 150 155 160	480
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val 165 170 175	528
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 180 185 190	576
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 195 200 205	624
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 210 215 220	672
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 225 230 235 240	720
gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly 245 250 255	768
gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met 260 265 270	816
atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His 275 280 285	864
gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val 290 295 300	912
cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr	960

305	310	315	320	
cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 325		330	335	1008
aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile 340	345		350	1056
gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 355	360		365	1104
tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser 370	375	380		1152
ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 385	390	395	400	1200
tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro 405	410		415	1248
gtg ctg gac tcc gac ggc tcc ttc ctc tac agc aag ctc acc gtg Val Leu Asp Ser Asp Gly Ser Phe Leu Tyr Ser Lys Leu Thr Val 420	425		430	1296
gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met 435	440		445	1344
cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tcc His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 450	455	460		1392
ccg ggg agc ggc ggg ctg aag atc gca gcc ttc aac atc cag aca ttt Pro Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe 465	470	475	480	1440
ggg gag acc aag atg tcc aat gcc acc ctc gtc agc tac att gtg cag Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln 485	490		495	1488
atc ctg agc cgc tac gac atc gcc ctg gtc cag gag gtc aga gac agc Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser 500	505		510	1536
cac ctg act gcc gtg ggg aag ctg ctg gac aac ctc aat cag gac gca His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala 515	520		525	1584
cca gac acc tat cac tac gtg gtc agt gag cca ctg gga cg aac agc Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser 530	535	540		1632
tat aag gag cgc tac ctg ttc gtg tac agg cct gac cag gtg tct gcg				1680

<210> 52

<211> 729

<212> PRT

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 heavy chain - DNase I fusion

&lt;400&gt; 52

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1															15

Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
														30	
20								25							

Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
															45
35							40								

Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
															60
50					55										

Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn
															80
65					70				75						

Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn
															95
85								90							

Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val
															110
100								105							

Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly
															125
115						120									

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
															140
130						135									

Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala
															160
145					150				155						

Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
															175
165						170									

Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
															190
180							185								

Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
															205
195						200									

Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

210	215	220
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys		
225                           230                           235                           240		
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly		
245                           250                           255		
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met		
260                           265                           270		
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His		
275                           280                           285		
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val		
290                           295                           300		
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr		
305                           310                           315                           320		
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly		
325                           330                           335		
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile		
340                           345                           350		
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val		
355                           360                           365		
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser		
370                           375                           380		
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu		
385                           390                           395                           400		
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro		
405                           410                           415		
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val		
420                           425                           430		
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met		
435                           440                           445		

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 450 455 460

Pro Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe  
 465 470 475 480

Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln  
 485 490 495

Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser  
 500 505 510

His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala  
 515 520 525

Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser  
 530 535 540

Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala  
 545 550 555 560

Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp  
 565 570 575

Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr  
 580 585 590

Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp  
 595 600 605

Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln  
 610 615 620

Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala  
 625 630 635 640

Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp  
 645 650 655

Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr  
 660 665 670

Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met  
 675 680 685

Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe  
 690 695 700

Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp  
 705 710 715 720

His Tyr Pro Val Glu Val Met Leu Lys  
 725

<210> 53

<211> 2226

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 53		
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gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg gggcctcagt gaagggtgtcc	120	
tgcaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180	
ggaaagggcc tcgagtggtt cgagagatt ttacctggaa gtaataattc tagatacaat	240	
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300	
gagctcagca gcctgaggc tgaggacaca gccgtctatt acttgcaag atcctacgac	360	
tttgcctggc ttgcttactg gggccaagg actctggtca cagtctcctc agcctccacc	420	
aagggccat cggctttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480	
gccctggct gcctggtcaa ggactacttc cccgaaccgg tgacgggtgc gtggactca	540	
ggcgccctga ccagcggcgt gcacacccttc ccggctgtcc tacagtctc aggactctac	600	
tccctcagca gcgtggtgac cgtccctcc agcagctgg gcacccagac ctacatctgc	660	
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720	
gacaaaactc acacatgccc accgtgccca gcacctgaac tcctgggggg accgtcagtc	780	
ttcctttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	840	
tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac	900	
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac	960	

cgtgtggtca	gcgtcctcac	cgtcctgcac	caggactggc	tgaatggcaa	ggagtacaag	1020
tgcaaggct	ccaacaaagc	cctcccagcc	cccatcgaga	aaaccatctc	caaagccaa	1080
ggcagcccc	gagaaccaca	ggtgtacacc	ctgccccat	cccggatga	gctgaccaag	1140
aaccaggta	gcctgacctg	cctggtaaaa	ggcttctatc	ccagcgacat	cgcgtggag	1200
tggagagca	atgggcagcc	ggagaacaac	tacaagacca	cgcctccgt	gctggactcc	1260
gacggctcct	tttcctcta	cagcaagctc	accgtggaca	agagcaggtg	gcagcagggg	1320
aacgtcttct	catgctccgt	gatgcatgag	gctctgcaca	accactacac	gcagaagagc	1380
ctctccctgt	ctccggtaa	agggagcggc	gggctgaaga	tcgcagcctt	caacatccag	1440
acatttgggg	agaccaagat	gtccaatgcc	accctcgta	gctacattgt	gcagatcctg	1500
agccgctacg	acatcgccct	ggtccaggag	gtcagagaca	gccacctgac	tgccgtgggg	1560
aagctgctgg	acaacctcaa	tcaggacgca	ccagacacct	atcactacgt	ggtcagttag	1620
ccactgggac	ggaacagcta	taaggagcgc	tacctgttcg	tgtacaggcc	tgaccaggtg	1680
tctgcggtgg	acagctacta	ctacgatgat	ggctgcgagc	cctgcggaa	cgacaccttc	1740
aaccgagagc	cagccattgt	caggttcttc	tcccggttca	cagaggtcag	ggagttgcc	1800
attgttcccc	tgcattgcggc	cccggggac	gcagtagccg	agatcgacgc	tctctatgac	1860
gtctacctgg	atgtccaaga	gaaatggggc	ttggaggacg	tcatgttgat	ggcgacttc	1920
aatgcgggct	gcagctatgt	gagaccctcc	cagtggtcat	ccatccgcct	gtggacaagc	1980
cccaccttcc	agtggctgat	ccccgacagc	gctgacacca	cagctacacc	cacgcactgt	2040
gcctatgaca	ggatcgttgt	tgcaggatg	ctgctccgag	ggccgttgt	tcccgactcg	2100
gctcttcct	ttaacttcca	ggctgcctat	ggcctgagtg	accaactggc	ccaagccatc	2160
agtgaccact	atccagtgga	ggtgatgctg	aagggggcg	gaccaaaaaa	gaagcgcaag	2220
gtttga						2226

<210> 54

<211> 2226

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<220>

<221> CDS

<222> (1) .. (2226)

<223>

<400> 54  
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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
1 5 10 15  
  
gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag 96  
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
20 25 30  
  
cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc 144  
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45  
  
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc 192  
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60  
  
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat 240  
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn  
65 70 75 80  
  
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac 288  
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn  
85 90 95  
  
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca tcc aca aac 336  
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
100 105 110  
  
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc 384  
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
115 120 125  
  
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg 432  
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
130 135 140  
  
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg 480  
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
145 150 155 160  
  
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg 528  
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
165 170 175  
  
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct 576  
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
180 185 190

gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 195 200 205	624
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 210 215 220	672
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 225 230 235 240	720
gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly 245 250 255	768
gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met 260 265 270	816
atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His 275 280 285	864
gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val 290 295 300	912
cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr 305 310 315 320	960
cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 325 330 335	1008
aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile 340 345 350	1056
gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 355 360 365	1104
tac acc ctg ccc cca tcc ccg gat gag ctg acc aag aac cag gtc agc Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser 370 375 380	1152
ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 385 390 395 400	1200
tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro 405 410 415	1248
gtg ctg gac tcc gac ggc tcc ttc ctc tac agc aag ctc acc gtg Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val	1296

420	425	430	
gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met 435	440	445	1344
cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 450	455	460	1392
ccg ggt aaa ggg agc ggc ggg ctg aag atc gca gcc ttc aac atc cag Pro Gly Lys Gly Ser Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln 465	470	475	1440
aca ttt ggg gag acc aag atg tcc aat gcc acc ctc gtc agc tac att Thr Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile 485	490	495	1488
gtg cag atc ctg agc cgc tac gac atc gcc ctg gtc cag gag gtc aga Val Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg 500	505	510	1536
gac agc cac ctg act gcc gtg ggg aag ctg ctg gac aac ctc aat cag Asp Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln 515	520	525	1584
gac gca cca gac acc tat cac tac gtg gtc agt gag cca ctg gga cg Asp Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg 530	535	540	1632
aac agc tat aag gag cgc tac ctg ttc gtg tac agg cct gac cag gtg Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val 545	550	555	1680
tct gcg gtg gac agc tac tac tac gat gat ggc tgc gag ccc tgc ggg Ser Ala Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly 565	570	575	1728
aac gac acc ttc aac cga gag cca gcc att gtc agg ttc ttc tcc cg Asn Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg 580	585	590	1776
ttc aca gag gtc agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg Phe Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro 595	600	605	1824
ggg gac gca gta gcc gag atc gac gct ctc tat gac gtc tac ctg gat Gly Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp 610	615	620	1872
gtc caa gag aaa tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc Val Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe 625	630	635	1920
aat gcg ggc tgc agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg 645	650	655	1968
ctg tgg aca agc ccc acc ttc cag tgg ctg atc ccc gac agc gct gac			2016

Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp			
660	665	670	
acc aca gct aca ccc acg cac tgt gcc tat gac agg atc gtg gtt gca			2064
Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala			
675	680	685	
ggg atg ctg ctc cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt			2112
Gly Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe			
690	695	700	
aac ttc cag gct gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc			2160
Asn Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile			
705	710	715	720
agt gac cac tat cca gtg gag gtg atg ctg aag ggg ggc gga ccc aaa			2208
Ser Asp His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Gly Pro Lys			
725	730	735	
aag aag cgc aag gtt tga			2226
Lys Lys Arg Lys Val			
740			

&lt;210&gt; 55

&lt;211&gt; 741

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 heavy chain - DNase I fusion

&lt;400&gt; 55

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly			
1	5	10	15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys			
20	25	30	

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe			
35	40	45	

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu			
50	55	60	

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn			
65	70	75	80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn  
 85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
 115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 355 360 365

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
 370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
 420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 450 455 460

Pro Gly Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln  
 465 470 475 480

Thr Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile  
 485 490 495

Val Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg  
 500 505 510

Asp Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln  
 515 520 525

Asp Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg  
 530 535 540

Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val

545	550	555	560
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Ser Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly			
565	570	575	

Asn Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg			
580	585	590	

Phe Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro			
595	600	605	

Gly Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp			
610	615	620	

Val Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe			
625	630	635	640

Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg			
645	650	655	

Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp			
660	665	670	

Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala			
675	680	685	

Gly Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe			
690	695	700	

Asn Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile			
705	710	715	720

Ser Asp His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Gly Pro Lys			
725	730	735	

Lys Lys Arg Lys Val			
740			

<210> 56

<211> 2223

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 heavy chain - DNase I fusion

<400> 56	
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt ccactcccaag	60
gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg gggcctcagt gaaggtgtcc	120
tgcaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
gaaagggcc tcgagtggtt cgagagatt ttacctggaa gtaataattc tagataaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgccttgtt ttgcttactg gggccaaggg actctggtca cagtcctc caccctccacc	420
aagggccat cggcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480
gccctggct gcctggcaa ggactacttc cccgaaccgg tgacgggtgc gtggactca	540
ggcgccctga ccagcggcgt gcacaccccttc ccggctgtcc tacagtcctc aggactctac	600
tccctcagca gcgtggtgac cgtccctcc agcagcttgg gcacccagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720
gacaaaactc acacatgccc accgtgccca gcacccgttac tcctgggggg accgtcagtc	780
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	840
tgcgtgggg tggacgtgag ccacgaagac cctgaggta agttcaactg gtacgtggac	900
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac	960
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag	1020
tgcagggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa	1080
ggcagcccc gagaaccaca ggtgtacacc ctgccccat cccggatga gctgaccaag	1140
aaccaggta gcctgacctg cctggtaaa ggcttctatc ccagcgacat cgccgtggag	1200
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctccgt gctggactcc	1260
gacggctcct tttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg	1320
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc	1380
ctctccctgt ctccgaaggg gagcggcggg ctgaagatcg cagcattcaa catccagaca	1440
tttggggaga ccaagatgtc caatgccacc ctcgtcagct acattgtgca gatcctgagc	1500
cgctacgaca tcgcccgtt ccaggaggtc agagacagcc acctgactgc cgtggggaaag	1560

ctgctggaca acctcaatca ggacgcacca gacacctatc actacgtggt cagttagcca 1620  
 ctgggacgga acagctataa ggagcgctac ctgttcgtgt acaggcctga ccaggtgtct 1680  
 gcgggtggaca gctactacta cgatgatggc tgcgagccct gcgggaacga cacccttcaac 1740  
 cgagagccag ccattgtcag gttcttctcc cggttcacag aggtcaggaa gtttgccatt 1800  
 gttcccctgc atgcggcccc gggggacgca gtagccgaga tcgacgctct ctatgacgtc 1860  
 tacctggatg tccaagagaa atggggcttg gaggacgtca tggtgatggg cgacttcaat 1920  
 gcgggctgca gctatgtgag accctccca ggtcatcca tccgcctgtg gacaagcccc 1980  
 accttccagt ggctgatccc cgacagcgct gacaccacag ctacacccac gcactgtgcc 2040  
 tatgacagga tcgtggttgc agggatgctg ctccgagggg ccgttgttcc cgactcggct 2100  
 cttccctta acttccaggc tgcctatggc ctgagtgacc aactggccca agccatcagt 2160  
 gaccactatc cagtggaggt gatgctgaag gggggcggac ccaaaaagaa gcgcaaggaa 2220  
 tga 2223

<210> 57

<211> 2223

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<220>

<221> CDS

<222> (1)..(2223)

<223>

<400> 57

atg	gga	tgg	agc	tgt	atc	atc	ctc	ttc	ttg	gta	gca	aca	gct	aca	ggt	48
Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly	
1															15	

gtc	cac	tcc	cag	gtg	cag	ctg	gtg	cag	tct	ggg	gca	gag	gtg	aaa	aag	96
Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	
															30	

cct	ggg	gcc	tca	gtg	aag	gtg	tcc	tgc	aag	gct	tct	ggc	tac	acc	ttc	144
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
35						40					45					
agt	gcc	tac	tgg	ata	gag	tgg	gtg	cgc	cag	gct	cca	gga	aag	ggc	ctc	192
Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
50						55					60					
gag	tgg	gtc	gga	gag	att	tta	cct	gga	agt	aat	aat	tct	aga	tac	aat	240
Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn	
65						70				75			80			
gag	aag	ttc	aag	ggc	cga	gtg	aca	gtc	act	aga	gac	aca	tcc	aca	aac	288
Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn	
85								90				95				
aca	gcc	tac	atg	gag	ctc	agc	agc	ctg	agg	tct	gag	gac	aca	gcc	gtc	336
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
100								105				110				
tat	tac	tgt	gca	aga	tcc	tac	gac	ttt	gcc	tgg	ttt	gct	tac	tgg	ggc	384
Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly	
115							120				125					
caa	ggg	act	ctg	gtc	aca	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	432
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	
130						135				140						
gtc	ttc	ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcf	480
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	
145						150				155			160			
gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	528
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	
165								170				175				
tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	576
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	
180							185				190					
gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	624
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
195							200				205					
ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	672
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	
210							215			220						
aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt	720
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	
225							230			235			240			
gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	ctc	ctg	ggg	768
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	
245								250			255					
gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	816
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	
260							265			270						

atc tcc cg acc cct gag gtc aca tgc gtg gtg gac gtg agc cac Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His 275 280 285	864
gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val 290 295 300	912
cat aat gcc aag aca aag ccg cg gag gag cag tac aac agc acg tac His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr 305 310 315 320	960
cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 325 330 335	1008
aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile 340 345 350	1056
gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 355 360 365	1104
tac acc ctg ccc cca tcc cg gat gag ctg acc aag aac cag gtc agc Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser 370 375 380	1152
ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 385 390 395 400	1200
tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro 405 410 415	1248
gtg ctg gac tcc gac ggc tcc ttc ctc tac agc aag ctc acc gtg Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val 420 425 430	1296
gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met 435 440 445	1344
cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 450 455 460	1392
ccg aag ggg agc ggc ggg ctg aag atc gca gcc ttc aac atc cag aca Pro Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr 465 470 475 480	1440
ttt ggg gag acc aag atg tcc aat gcc acc ctc gtc agc tac att gtg Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val 485 490 495	1488
cag atc ctg agc cgc tac gac atc gcc ctg gtc cag gag gtc aga gac Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp 500 505 510	1536

agc cac ctg act gcc gtg ggg aag ctg ctg gac aac ctc aat cag gac Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp 515 520 525	1584
gca cca gac acc tat cac tac gtg gtc agt gag cca ctg gga cg <sup>g</sup> aac Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn 530 535 540	1632
agc tat aag gag cgc tac ctg ttc gtg tac agg cct gac cag gtg tct Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser 545 550 555 560	1680
gcg gtg gac agc tac tac tac gat gat ggc tgc gag ccc tgc ggg aac Ala Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn 565 570 575	1728
gac acc ttc aac cga gag cca gcc att gtc agg ttc ttc tcc cgg ttc Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe 580 585 590	1776
aca gag gtc agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly 595 600 605	1824
gac gca gta gcc gag atc gac gct ctc tat gac gtc tac ctg gat gtc Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val 610 615 620	1872
caa gag aaa tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc aat Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn 625 630 635 640	1920
gcg ggc tgc agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc ctg Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu 645 650 655	1968
tgg aca agc ccc acc ttc cag tgg ctg atc ccc gac agc gct gac acc Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr 660 665 670	2016
aca gct aca ccc acg cac tgt gcc tat gac agg atc gtg gtt gca ggg Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly 675 680 685	2064
atg ctg ctc cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn 690 695 700	2112
ttc cag gct gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc agt Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser 705 710 715 720	2160
gac cac tat cca gtg gag gtg atg ctg aag ggg ggc gga ccc aaa aag Asp His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Gly Pro Lys Lys 725 730 735	2208
aag cgc aag gtt tga Lys Arg Lys Val	2223

740

&lt;210&gt; 58

&lt;211&gt; 740

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 heavy chain - DNase I fusion

&lt;400&gt; 58

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1				5					10				15		

Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
						20		25					30		

Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
					35		40					45			

Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
					50		55		60						

Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn
					65		70		75			80			

Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn
					85		90		95						

Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val
					100			105				110			

Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly
					115		120			125					

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
					130		135			140					

Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala
					145		150			155			160		

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 355 360 365

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
 370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
 420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 450 455 460

Pro Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr  
 465 470 475 480

Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val  
 485 490 495

Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp  
 500 505 510

Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp  
 515 520 525

Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn  
 530 535 540

Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser  
 545 550 555 560

Ala Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn  
 565 570 575

Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe  
 580 585 590

Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly  
 595 600 605

Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val  
 610 615 620

Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn  
 625 630 635 640

Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu  
645 650 655

Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr  
660 665 670

Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly  
675 680 685

Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn  
690 695 700

Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser  
705 710 715 720

Asp His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Gly Pro Lys Lys  
725 730 735

Lys Arg Lys Val  
740

<210> 59

<211> 2220

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 59

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gtcagctgg tgcagtctgg ggcagaggtg aaaaagcctg ggcctcagt gaagggtgtcc 120  
tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca 180  
ggaaagggcc tcgagtggtt cgagagatt ttacctggaa gtaataattc tagatacaat 240  
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg 300  
gagctcagca gcctgaggc tgaggacaca gccgtctatt actgtgcaag atcctacgac 360  
tttgcctgggt ttgcttactg gggccaagg actctggtca cagtctcctc aqccctccacc 420

aaggccat cggcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480
gccctggct gcctggtaa ggactacttc cccgaaccgg tgacggtgac gtggaaactca	540
ggcgccctga ccagcggcgt gcacacccitc ccggctgtcc tacagtccctc aggactctac	600
tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720
gacaaaactc acacatgccc accgtgccc gcacctgaac tcctgggggg accgtcagtc	780
ttcctcttcc ccccaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	840
tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac	900
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac	960
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag	1020
tgcaaggctt ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa	1080
gggcagcccc gagaaccaca ggtgtacacc ctgccccat cccggatga gctgaccaag	1140
aaccaggta gcctgacctg cctggtaaaa ggcttctatc ccagcgacat cgccgtggag	1200
tggagagca atgggcagcc ggagaacaac tacaagacca cgcctccgt gctggactcc	1260
gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg	1320
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc	1380
ctctccctgt ccccgggag cggcgggctg aagatcgac cttcaacat ccagacattt	1440
ggggagacca agatgtccaa tgccaccctc gtcagctaca ttgtgcagat cctgagccgc	1500
tacgacatcg ccctggtcca ggaggtcaga gacagccacc tgactgccgt gggaaagctg	1560
ctggacaacc tcaatcagga cgcaccagac acctatcact acgtggtcag tgagccactg	1620
ggacggaaca gctataagga gcgctacctg ttcgtgtaca ggcctgacca ggtgtctg	1680
gtggacagct actactacga tcatggctgc gagccctgcg ggaacgacac cttcaaccga	1740
gagccagcca ttgtcagggtt cttctccgg ttcacagagg tcagggagtt tgccattgtt	1800
ccctgcattt cggccccggg ggacgcagta gccgagatcg acgctctcta tgacgtctac	1860
ctggatgtcc aagagaaatg gggcttggag gacgtcatgt tcatggcga cttcaatgcg	1920
ggctgcagct atgtgagacc ctcccagtgg tcatccatcc gcctgtggac aagccccacc	1980
ttccagtgcc tcatggccaa cagcgctgac accacagcta cacccacgca ctgtgcctat	2040
gacaggatcg tggttgcagg gatgctgctc cgagggggccg ttgttcccga ctcggcttt	2100
cccttaact tccaggctgc cttatggcctg agtgcaccaac tggcccaagc catcagtgc	2160
cactatccag tggaggtgat gctgaagggg ggcggaccca aaaagaagcg caaggttga	2220

<210> 60  
<211> 2220  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Humanised HMFG1 heavy chain - DNase I fusion  
<220>  
<221> CDS  
<222> (1)..(220)  
<223>  
  
<400> 60  
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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
1 5 10 15  
  
gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag 96  
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
20 25 30  
  
cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc 144  
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45  
  
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc 192  
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60  
  
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat 240  
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn  
65 70 75 80  
  
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac 288  
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn  
85 90 95  
  
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc 336  
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
100 105 110  
  
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc 384  
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
115 120 125

caa	ggg	act	ctg	gtc	aca	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg		432
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser		
130					135							140					
gtc	ttc	ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg		480
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala		
145					150						155				160		
gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg		528
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val		
					165					170				175			
tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct		576
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala		
					180					185				190			
gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg		624
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val		
					195				200			205					
ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac		672
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His		
					210				215			220					
aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt		720
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys		
					225				230			235			240		
gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	ctc	ctg	ggg		768
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly		
					245				250			255					
gga	ccg	tca	gtc	tcc	ctc	tcc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg		816
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met		
					260				265			270					
atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac		864
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His		
					275				280			285					
gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg		912
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val		
					290				295			300					
cat	aat	gcc	aag	aca	aag	ccg	ccg	gag	gag	cag	tac	aac	agc	acg	tac		960
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr		
					305				310			315			320		
cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc		1008
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly		
					325				330			335					
aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	atc		1056
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile		
					340				345			350					
gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg		1104
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val		
					355				360			365					

tac acc ctg ccc cca tcc cg <sup>g</sup> gat gag ctg acc aag aac cag gtc agc Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser 370 375 380	1152
ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 385 390 395 400	1200
tgg gag agc aat ggg cag cc <sup>g</sup> gag aac aac tac aag acc acg cct ccc Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro 405 410 415	1248
gtg ctg gac tcc gac ggc tcc ttc ctc tac agc aag ctc acc gtg Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val 420 425 430	1296
gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met 435 440 445	1344
cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tcc His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 450 455 460	1392
ccg ggg agc ggc ggg ctg aag atc gca gcc ttc aac atc cag aca ttt Pro Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe 465 470 475 480	1440
ggg gag acc aag atg tcc aat gcc acc ctc gtc agc tac att gtg cag Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln 485 490 495	1488
atc ctg agc cgc tac gac atc gcc ctg gtc cag gag gtc aga gac agc Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser 500 505 510	1536
cac ctg act gcc gtg ggg aag ctg ctg gac aac ctc aat cag gac gca His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala 515 520 525	1584
cca gac acc tat cac tac gtg gtc agt gag cca ctg gga cg <sup>g</sup> aac agc Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser 530 535 540	1632
tat aag gag cgc tac ctg ttc gtg tac agg cct gac cag gtg tct gc <sup>g</sup> Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala 545 550 555 560	1680
gtg gac agc tac tac gat gat ggc tgc gag ccc tgc ggg aac gac Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp 565 570 575	1728
acc ttc aac cga gag cca gcc att gtc agg ttc ttc tcc cg <sup>g</sup> ttc aca Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr 580 585 590	1776
gag gtc agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg gac Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp	1824

595	600	605	
gca gta gcc gag atc gac gct ctc tat gac gtc tac ctg gat gtc caa Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln			1872
610	615	620	
gag aaa tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc aat gcg Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala			1920
625	630	635	640
ggc tgc agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc ctg tgg Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp			1968
645	650		655
aca agc ccc acc ttc cag tgg ctg atc ccc gac agc gct gac acc aca Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr			2016
660	665		670
gct aca ccc acg cac tgt gcc tat gac agg atc gtg gtt gca ggg atg Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met			2064
675	680		685
ctg ctc cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac ttc Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe			2112
690	695		700
cag gct gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc agt gac Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp			2160
705	710		715
cac tat cca gtg gag gtg atg ctg aag ggg ggc gga ccc aaa aag aag His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Pro Lys Lys Lys			2208
725	730		735
cgc aag gtt tga Arg Lys Val			2220

<210> 61

<211> 739

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 61

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
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Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 50 55 60

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn  
 65 70 75 80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn  
 85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
 115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 355 360 365

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
 370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
 420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 450 455 460

Pro Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe  
 465 470 475 480

Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln  
 485 490 495

Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser  
 500 505 510

His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala  
 515 520 525

Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser  
 530 535 540

Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala  
 545 550 555 560

Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp  
 565 570 575

Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr  
 580 585 590

Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp  
 595 600 605

Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln  
 610 615 620

Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala  
 625 630 635 640

Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp  
 645 650 655

Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr  
 660 665 670

Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met  
 675 680 685

Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe  
 690 695 700

Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp  
 705 710 715 720

His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Pro Lys Lys

725

730

735

Arg Lys Val

&lt;210&gt; 62

&lt;211&gt; 1548

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;400&gt; 62

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gtgcagctgg	tgcagtctgg	ggcagaggtg	aaaaagcctg	gggcctcagt	gaagggtgtcc	120
tgcaaggctt	ctggctacac	cttcagtgcc	tactggatag	agtgggtgcg	ccaggctcca	180
ggaaagggcc	tcgagtgggt	cggagagatt	ttacctggaa	gtaataattc	tagataacaat	240
gagaagtca	agggccgagt	gacagtcact	agagacacat	ccacaaacac	agcctacatg	300
gagctcagca	gcctgaggtc	tgaggacaca	gccgtctatt	acttgcaag	atcctacgac	360
tttgcctgg	ttgcttactg	gggccaagg	actctggtca	cagtctcctc	agcctccacc	420
aagggccc	cggtcttccc	cctggcaccc	tcctccaaga	gcacctctgg	gggcacagcg	480
gccctgg	gcctggtaa	ggactacttc	cccgaaccgg	tgacgggtgc	gtggaactca	540
ggcgcc	ccagcggcgt	gcacaccttc	ccggctgtcc	tacagtctc	aggactctac	600
tccctc	gcgtggtgac	cgtccctcc	agcagcttgg	gcacccagac	ctacatctgc	660
aacgt	acaagccc	caacaccaag	gtggacaaga	aagttgagcc	caaatcttgt	720
gacaaa	acacatgccc	accgtgccc	gcacctgaag	gcgggctgaa	gatcgagcc	780
ttcaacatcc	agacatttgg	ggagaccaag	atgtccatg	ccaccctcg	cagctacatt	840
gtgcagatcc	tgagccgcta	cgacatcgcc	ctggtccagg	aggcagaga	cagccacctg	900
actgccgtgg	ggaagctgct	ggacaacctc	aatcaggacg	caccagacac	ctatcactac	960
gtggtcagt	agccactgg	acgaaacagc	tataaggac	gctacctgtt	cgtgtacagg	1020
cctgaccagg	tgtctgcggt	ggacagctac	tactacgatg	atggctgcga	gccctgcggg	1080
aacgacac	tcaaccgaga	gccagccatt	gtcaggttct	tctcccggtt	cacagaggtc	1140

agggagttg ccattgttcc cctgcatgcg gccccggggg acgcaagtagc cgagatcgac 1200  
 gctctctatg acgtctacctt ggatgtccaa gagaaatggg gcttggagga cgtcatgtt 1260  
 atgggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtggtc atccatccgc 1320  
 ctgtggacaa gccccacattt ccagtggctg atccccgaca gcgcgtgacac cacagctaca 1380  
 cccacgcact gtgcctatga caggatcgta gttgcaggga tgctgctccg agggggccgtt 1440  
 gttcccgact cggctttcc cttaacttc caggctgcct atggcctgag tgaccaactg 1500  
 gcccaaggcca tcagtgacca ctatccagtg gaggtgatgc tgaagtga 1548

<210> 63

<211> 1548

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 63  
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 gtgcagctgg tgcagttctgg ggcagaggtg aaaaagcctg gggcctcagt gaaggtgtcc 120  
 tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca 180  
 ggaaagggcc tcgagttgggt cggagagatt ttacctggaa gtaataattc tagatacaat 240  
 gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg 300  
 gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac 360  
 tttgcctggc ttgcttactg gggccaagg actctggtca cagtcctc agcctccacc 420  
 aaggggccat cggctttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 480  
 gccctggct gcctggtaa ggactacttc cccgaaccgg tgacgggtgc gtggaaactca 540  
 ggcgcctga ccagcggcgt gcacacccctc ccggctgtcc tacagtcctc aggactctac 600  
 tccctcagca gcgtggtgac cgtccctcc agcagcttgg gcacccagac ctacatctgc 660  
 aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 720  
 gacaaaactc acacatgtcc accgtgtcca gcaccagagg gcgggctgaa gatcgagcc 780  
 ttcaacatcc agacatttgg ggagaccaag atgtccatg ccaccctcgt cagctacatt 840

gtgcagatcc tgagccgcta cgacatcgcc ctgggccagg aggtcagaga cagccacctg	900
actgccgtgg ggaagctgct ggacaacctc aatcaggacg caccagacac ctatcactac	960
gtggtcagtg agccactggg acgaaacagc tataaggagc gctacctgtt cgtgtacagg	1020
cctgaccagg tgtctgcgtt ggacagctac tactacgtg atggctgcga gccctgcggg	1080
aacgacacct tcaaccgaga gccagccatt gtcaggttct tctcccggtt cacagaggtc	1140
agggagtttgcattgttcc cctgcatgcg gccccgggg acgcagtagc cgagatcgac	1200
gctctctatg acgtctacctt ggatgtccaa gagaaatggg gcttggagga cgtcatgttgc	1260
atgggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtggtc atccatccgc	1320
ctgtggacaa gccccacatt ccagtggctg atccccgaca gcgcgtgacac cacagctaca	1380
cccacgcact gtgccttatga caggatcggt gttgcaggga tgctgctccg agggggccgtt	1440
gttcccgact cggctttcc cttaacttc caggctgcct atggcctgag tgaccaactg	1500
gcccaagcca tcagtgacca ctatccagtg gaggtgatgc tgaagtga	1548

<210> 64

<211> 1557

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

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cactccagg tgcagctggt gcagtctggg gcagaggtga aaaagcctgg ggcctcagtg	120
aagggtgcct gcaaggcttc tggctacacc ttcaagtgcct actggataga gtgggtgcgc	180
caggctccag gaaaggccct cgagtgggtc ggagagattt tacctggaag taataattct	240
agatacaatg agaagttcaa ggcccgagtg acagtcaacta gagacacatc cacaacaca	300
gcctacatgg agctcagcag cctgagggtct gaggacacag ccgtctatta ctgtgcaaga	360
tcctacgact ttgcctgggt tgcttactgg gccaaggga ctctggcac agtctcctca	420
gcctccacca agggccatc ggtttcccc ctggcaccct cctccaagag cacctctggg	480
ggcacagcgg ccctggctg cctggtaag gactacttcc ccgaaccgggt gacgggtgtcg	540
tggaaactcag gcccctgac cagcggcgtg cacaccccttcc cggctgtcct acagtcctca	600

ggactctact	ccctcagcag	cgtggtgacc	gtgcctcca	gcagcttggg	cacccagacc	660
tacatctgca	acgtgaatca	caagcccagc	aacaccaagg	tggacaagaa	agttgagccc	720
aaatcttgtg	acaaaactca	cacatgtcca	ccgtgtccag	caccagaggg	cgggctgaag	780
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tatcactacg	tggtcagtga	gccactggga	cggaacagct	ataaggagcg	ctacctgttc	1020
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ccctgcggga	acgacacctt	caaccgagag	ccagccattg	tcaggttctt	ctcccggttc	1140
acagaggtca	gggagttgc	cattgttccc	ctgcatgcgg	ccccggggga	cgcagtagcc	1200
gagatcgacg	ctctctatga	cgtctacctg	gatgtccaag	agaaatgggg	cttggaggac	1260
gtcatgtga	tggcgactt	caatgcgggc	tgcagctatg	tgagaccctc	ccagtggta	1320
tccatccgcc	tgtggacaag	ccccaccttc	cagtggctga	tccccgacag	cgctgacacc	1380
acagctacac	ccacgcactg	tgcctatgac	aggatcgtgg	ttgcagggat	gctgctccga	1440
ggggccgttg	ttcccgactc	ggctcttccc	tttaacttcc	aggctgccta	tggcctgagt	1500
gaccaactgg	cccaagccat	cagtgaccac	tatccagtgg	aggtgatgct	gaagtga	1557

<210> 65

<211> 1548

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<220>

<221> CDS

<222> (1)..(1548)

<223>

<400> 65

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gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys 20 25 30	96
cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe 35 40 45	144
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu 50 55 60	192
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn 65 70 75 80	240
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn 85 90 95	288
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val 100 105 110	336
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly 115 120 125	384
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser 130 135 140	432
gtc ttc ccc ctg gca ccc tcc aag agc acc tct ggg ggc aca gcg Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala 145 150 155 160	480
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val 165 170 175	528
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 180 185 190	576
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 195 200 205	624
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 210 215 220	672
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 225 230 235 240	720

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ggc ggg ctg Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Gly Gly Leu 245 250 255	768
aag atc gca gcc ttc aac atc cag aca ttt ggg gag acc aag atg tcc Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys Met Ser 260 265 270	816
aat gcc acc ctc gtc agc tac att gtg cag atc ctg agc cgc tac gac Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp 275 280 285	864
atc gcc ctg gtc cag gag gtc aga gac agc cac ctg act gcc gtg ggg Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val Gly 290 295 300	912
aag ctg ctg gac aac ctc aat cag gac gca cca gac acc tat cac tac Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His Tyr 305 310 315 320	960
gtg gtc agt gag cca ctg gga cg aac agc tat aag gag cgc tac ctg Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr Leu 325 330 335	1008
tcc gtc tac agg cct gac cag gtg tct gcg gtg gac agc tac tac tac Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr Tyr Tyr 340 345 350	1056
gat gat ggc tgc gag ccc tgc ggg aac gac acc ttc aac cga gag cca Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg Glu Pro 355 360 365	1104
gcc att gtc agg ttc tcc tcc cgg ttc aca gag gtc agg gag ttt gcc Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu Phe Ala 370 375 380	1152
att gtt ccc ctg cat gcg gcc ccg ggg gac gca gta gcc gag atc gac Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile Asp 385 390 395 400	1200
gct ctc tat gac gtc tac ctg gat gtc caa gag aaa tgg ggc ttg gag Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu Glu 405 410 415	1248
gac gtc atg ttg atg ggc gac ttc aat gcg ggc tgc agc tat gtg aga Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg 420 425 430	1296
ccc tcc cag tgg tca tcc atc cgc ctg tgg aca agc ccc acc ttc cag Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln 435 440 445	1344
tgg ctg atc ccc gac agc gct gac acc aca gct aca ccc acg cac tgt Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr His Cys 450 455 460	1392
gcc tat gac agg atc gtg gtt gca ggg atg ctg ctc cga ggg gcc gtt Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly Ala Val	1440

gtt ccc gac tcg gct ctt ccc ttt aac ttc cag gct gcc tat ggc ctg Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly Leu 485	470	475	480	
				1488
agt gac caa ctg gcc caa gcc atc agt gac cac tat cca gtg gag gtg Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val Glu Val 500	490	495		
				1536
atg ctg aag tga Met Leu Lys 515				1548
<210> 66				
<211> 515				
<212> PRT				
<213> Artificial Sequence				
<220>				
<223> Humanised HMFG1 Fd - DNase I fusion				
<400> 66				
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Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys 20 25 30				
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe 35 40 45				
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu 50 55 60				
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn 65 70 75 80				
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn 85 90 95				
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val 100 105 110				

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
 115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Gly Gly Leu  
 245 250 255

Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys Met Ser  
 260 265 270

Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp  
 275 280 285

Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val Gly  
 290 295 300

Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His Tyr  
 305 310 315 320

Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr Leu  
 325 330 335

Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr Tyr Tyr  
 340 345 350

Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg Glu Pro  
 355 360 365

Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu Phe Ala  
 370 375 380

Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile Asp  
 385 390 395 400

Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu Glu  
 405 410 415

Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg  
 420 425 430

Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln  
 435 440 445

Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr His Cys  
 450 455 460

Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly Ala Val  
 465 470 475 480

Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly Leu  
 485 490 495

Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val Glu Val  
 500 505 510

Met Leu Lys  
 515

<210> 67

<211> 1566

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 67  
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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca  
gaaagggcc tcgagtggtt cgagagatt ttacctggaa gtaataattc tagataacaat  
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg 120  
gagctcagca gcctgaggtc tgaggacaca gccgtctatt acttgcaag atcctacgac  
tttgcctgg ttgcttactg gggccaagg actctggtca cagtcctcacc agcctccacc  
aagggccat cggcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 180  
gccctggct gcctggtcaa ggactacttc cccgaaccgg tgacgggtgc gtggactca  
ggcgccctga ccagcggcgt gcacacccctc cggctgtcc tacagtcctc aggactctac  
tccctcagca gcgtggtgac cgtccctcc agcagcttgg gcacccagac ctacatctgc 240  
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt  
gacaaaactc acacatgctg tgtggagtgc ccaccgtgcc cagcacctga agggagcggc  
gggctgaaga tcgcagcctt caacatccag acatttgggg agaccaagat gtccatgcc 300  
accctcgta gctacattgt gcagatcctg agccgctacg acatcgccct ggtccaggag  
gtcagagaca gccacctgac tgccgtgggg aagctgtgg acaaccta a ctaggacgca  
ccagacacct atcactacgt ggtcagttag ccactggac ggaacagcta taaggagcgc 360  
tacctgttcg tgtacaggcc tgaccaggtg tctgcgggtgg acagctacta ctacgatgat  
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tcccggttca cagaggtcag ggagtttgc attgtcccc tgcattgcggc cccgggggac 420  
gcagtagccg agatcgacgc tctctatgac gtctacctgg atgtccaaga gaaatggggc  
ttggaggacg tcatgttgat gggcgacttc aatgcgggtc gcagctatgt gagaccctcc  
cagtggtcat ccatccgcct gtggacaagc cccacccctc agtggctgat ccccgacagc  
gctgacacca cagctacacc cacgcactgt gcctatgaca ggatcgtgg tgcaggatg 480  
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ggcctgagtg accaactggc ccaagccatc agtaccact atccagtgaa ggtgatgctg  
aagtga 540  
1566

&lt;211&gt; 1566

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

<400> 68		
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tgcaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180	
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagataacaat	240	
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300	
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360	
tttgcctggc ttgcttactg gggccaaggg actctggtca cagtctcctc agcctccacc	420	
aaggggccat cggcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480	
gccctggct gcctggcaa ggactacttc cccgaaccgg tgacgggtgc gtggaactca	540	
ggcgccctga ccagcggcgt gcacacccctc ccggctgtcc tacagtctc aggactctac	600	
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gacaaaactc acacatgctg tgcgttgtt ccaccgtgtc cagcaccaga gggagcggc	780	
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accctcgta gctacattgt gcagatctgt agccgctacg acatcgccct ggtccaggag	900	
gtcagagaca gccacctgac tgccgtgggg aagctgtgg acaaccta a tcaggacgca	960	
ccagacacct atcactacgt ggtcagttag ccactggac ggaacagcta taaggagcgc	1020	
tacctgttgc tgtacaggcc tgaccaggtg tctgcgggtgg acagctacta ctacgatgt	1080	
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gcagtagccg agatcgacgc tctctatgac gtctacctgg atgtccaaga gaaatggggc	1260	
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cagtggtcat ccatccgcct gtggacaagc cccacccctcc agtggctgat ccccgacagc	1380	

gctgacacca cagctacacc cacgcactgt gcctatgaca ggatcgtgg tgcaggatg 1440  
 ctgctccgag gggccgttgt tcccgactcg gctttccct ttaacttcca ggctgcctat 1500  
 ggcctgagt accaactggc ccaagccatc agtaccact atccagtgg agtgatgctg 1560  
 aagtga 1566

<210> 69

<211> 1575

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 69  
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 caggctccag gaaaggcct cgagtggtc ggagagattt tacctggaa taataattct 240  
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 gcctacatgg agctcagcag cctgaggtct gaggacacag ccgtctatta ctgtgcaaga 360  
 tcctacgact ttgcctggtt tgcttactgg ggccaaggga ctctggtcac agtctcctca 420  
 gcctccacca agggcccatc ggtctcccc ctggcaccct cctccaagag cacctctgg 480  
 ggcacagcgg ccctggctg cctggtcaag gactactcc ccgaaccggg gacggtgtcg 540  
 tggaaactcag gcgcctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600  
 ggactctact ccctcagcag cgtggtgacc gtgcctcca gcagcttggg cacccagacc 660  
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720  
 aaatcttgtg acaaaaactca cacatgctgt gtcagtgtc caccgtgtcc agcaccagag 780  
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 caggacgcac cagacaccta tcactacgtg gtcagtgagc cactggacg gaacagctat 1020  
 aaggagcgct acctgttcgt gtacaggcct gaccaggtgt ctgcggtgga cagctactac 1080

## 100

tacgatgatg gctgcgagcc ctgcggaaac gacaccttca accgagagcc agccattgtc 1140  
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&lt;210&gt; 70

&lt;211&gt; 1566

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1566)

&lt;223&gt;

&lt;400&gt; 70

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt	48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag	96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35 40 45	

agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc	192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	

## 101

50	55	60	
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn			240
65	70	75	80
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn			288
85	90	95	
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val			336
100	105	110	
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly			384
115	120	125	
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser			432
130	135	140	
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala			480
145	150	155	160
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val			528
165	170	175	
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala			576
180	185	190	
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val			624
195	200	205	
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His			672
210	215	220	
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys			720
225	230	235	240
gac aaa act cac aca tgc tgt gtg gag tgc cca ccg tgc cca gca cct Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro			768
245	250	255	
gaa ggg agc ggc ggg ctg aag atc gca gcc ttc aac atc cag aca ttt Glu Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe			816
260	265	270	
ggg gag acc aag atg tcc aat gcc acc ctc gtc agc tac att gtg cag Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln			864
275	280	285	
atc ctg agc cgc tac gac atc gcc ctg gtc cag gag gtc aga gac agc			912

Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser			
290	295	300	
cac ctg act gcc gtg ggg aag ctg ctg gac aac ctc aat cag gac gca			960
His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala			
305	310	315	320
cca gac acc tat cac tac gtg gtc agt gag cca ctg gga cg aac agc			1008
Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser			
325	330	335	
tat aag gag cgc tac ctg ttc gtg tac agg cct gac cag gtg tct gcg			1056
Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala			
340	345	350	
gtg gac agc tac tac tac gat gat ggc tgc gag ccc tgc ggg aac gac			1104
Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp			
355	360	365	
acc ttc aac cga gag cca gcc att gtc agg ttc ttc tcc cg ttc aca			1152
Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr			
370	375	380	
gag gtc agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg gac			1200
Glu Val Arg Glu Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp			
385	390	395	400
gca gta gcc gag atc gac gct ctc tat gac gtc tac ctg gat gtc caa			1248
Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln			
405	410	415	
gag aaa tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc aat gcg			1296
Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala			
420	425	430	
ggc tgc agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc ctg tgg			1344
Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp			
435	440	445	
aca agc ccc acc ttc cag tgg ctg atc ccc gac agc gct gac acc aca			1392
Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr			
450	455	460	
gct aca ccc acg cac tgt gcc tat gac agg atc gtc gtt gca ggg atg			1440
Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met			
465	470	475	480
ctg ctc cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac ttc			1488
Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe			
485	490	495	
cag gct gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc agt gac			1536
Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp			
500	505	510	
cac tat cca gtg gag gtg atg ctg aag tga			1566
His Tyr Pro Val Glu Val Met Leu Lys			
515	520		

<210> 71

<211> 521

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 71

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1									10						15

Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
								25						30	

Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
													45		
35						40									

Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
									55						60
50															

Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn
															80
65						70				75					

Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn
									85				90		95

Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val
															110
			100					105							

Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly
															125
		115					120								

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
															140
									130						

Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala
															160
								145			155				

Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
															175
						165			170						

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240

Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro  
 245 250 255

Glu Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe  
 260 265 270

Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln  
 275 280 285

Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser  
 290 295 300

His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala  
 305 310 315 320

Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser  
 325 330 335

Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala  
 340 345 350

Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp  
 355 360 365

Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr  
 370 375 380

Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp  
 385 390 395 400

Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln

105

405

410

415

Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala  
420 425 430

Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp  
435 440 445

Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr  
450 455 460

Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met  
465 470 475 480

Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe  
485 490 495

Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp  
500 505 510

His Tyr Pro Val Glu Val Met Leu Lys  
515 520

<210> 72

<211> 1560

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 72

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tgcaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca 180

ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagataaat 240

gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg 300

gagctcagca gcctgaggc tgaggacaca gccgtctatt actgtgcaag atcctacgac 360

tttgcctgggt ttgcttactg gggccaaggg actctggtca cagtctcctc agcctccacc 420

aagggccat	cggctttccc	cctggcaccc	tcctccaaga	gcacctctgg	gggcacagcg	480
gccctggct	gcctggtcaa	ggactacttc	cccgaaccgg	tgacggtgtc	gtgaaactca	540
ggcgccctga	ccagcggcgt	gcacacccccc	ccggctgtcc	tacagtccctc	aggactctac	600
tccctcagca	gcgtggtgac	cgtgcctcc	agcagcttgg	gcacccagac	ctacatctgc	660
aacgtgaatc	acaagcccag	caacaccaag	gtggacaaga	aagttgagcc	caaatcttgt	720
gacaaaactc	acacatgctg	tgtggagtgc	ccaccgtgcc	cagcacctga	aggcgggctg	780
aagatcgtag	ccttcaacat	ccagacattt	ggggagacca	agatgtccaa	tgccaccctc	840
gtcagctaca	ttgtgcagat	cctgagccgc	tacgacatcg	ccctggtcca	ggaggtcaga	900
gacagccacc	tgactgccgt	gggaaagctg	ctggacaacc	tcaatcagga	cgcaccagac	960
acctatcact	acgtggtcag	tgagccactg	ggacggaaca	gctataagga	gcgttacctg	1020
ttcgtgtaca	ggcctgacca	ggtgtctgcg	gtggacagct	actactacga	tgtggctgc	1080
gagccctgcg	ggaacgacac	cttcaaccga	gagccagcca	ttgtcaggtt	cttctcccg	1140
ttcacagagg	tcagggagtt	tgccattgtt	cccctgcatt	cggccccggg	ggacgcagta	1200
gccgagatcg	acgctctcta	tgacgtctac	ctggatgtcc	aagagaaatg	gggttggag	1260
gacgtcatgt	tgtggcga	cttcaatgcg	ggctgcagct	atgtgagacc	ctcccagtgg	1320
tcatccatcc	gcctgtggac	aagccccacc	ttccagtggc	tgtccccga	cagcgctgac	1380
accacagcta	cacccacgca	ctgtgcctat	gacaggatcg	tggttgcagg	gatgctgctc	1440
cgaggggccg	ttgttcccga	ctcggtctt	cccttaact	tccaggctgc	ctatggcctg	1500
agtgaccaac	tggcccaagc	catcagtgac	cactatccag	tggaggtgat	gctgaagtga	1560

&lt;210&gt; 73

&lt;211&gt; 1560

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;400&gt; 73

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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtggt cgagagatt ttacctggaa gtaataattc tagataacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agctcacatg	300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt acttgcaag atcctacgac	360
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tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720
gacaaaactc acacatgctg tgcgagttt ccaccgtgtc cagcaccaga gggcgggctg	780
aagatcgca gcttcaacat ccagacattt gggagacca agatgtccaa tgccaccctc	840
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gagccctgcg ggaacgacac cttcaaccga gagccagcca ttgtcagggtt cttctcccg	1140
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cgagggggccg ttgttcccgaa ctcggcttt cccttaact tccaggctgc ctatggcctg	1500
agtgaccaac tggcccaagc catcagtgac cactatccag tggaggtgat gctgaagtga	1560

&lt;210&gt; 74

&lt;211&gt; 1569

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;400&gt; 74

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aagggtgcct	gcaaggcttc	tggctacacc	ttcagtgcct	actggataga	gtgggtgcgc	180
caggctccag	gaaagggcct	cgagtggtc	ggagagattt	tacctggaag	taataattct	240
agataacaatg	agaagttcaa	ggcccgagtg	acagtcacta	gagacacatc	cacaaacaca	300
gcctacatgg	agtcagcag	cctgaggtct	gaggacacag	ccgtcttatta	cttgcaaga	360
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atgctgtcc	gagggccgt	tgttcccgac	tcggcttcc	ccttaactt	ccaggctgcc	1500
tatggcctga	gtgaccaact	ggcccaagcc	atcagtgacc	actatccagt	ggaggtgatg	1560
ctgaagtga						1569

&lt;210&gt; 75

&lt;211&gt; 1560

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1560)

&lt;223&gt;

&lt;400&gt; 75

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt	48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1                       5                       10                       15	

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag	96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20                     25                       30	

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35                     40                       45	

agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc	192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
50                     55                       60	

gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat	240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn	
65                     70                       75                       80	

gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac	288
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn	
85                     90                       95	

aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
100                   105                       110	

tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc	384
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly	
115                   120                       125	

caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg	432
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Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	
130						135						140				
gtc	tcc	ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	480
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	
145						150					155				160	
gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	tcc	ccc	gaa	ccg	gtg	acg	gtg	528
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	
						165			170				175			
tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	tcc	ccg	gct	576
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	
						180			185				190			
gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	624
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Val	Thr	Val
						195			200				205			
ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	672
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	
						210			215				220			
aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt	720
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	
						225			230				235			240
gac	aaa	act	cac	aca	tgc	tgt	gtg	gag	tgc	cca	ccg	tgc	cca	gca	cct	768
Asp	Lys	Thr	His	Thr	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	
						245			250				255			
gaa	ggc	ggg	ctg	aag	atc	gca	gcc	ttc	aac	atc	cag	aca	ttt	ggg	gag	816
Glu	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	Thr	Phe	Gly	Glu	
						260			265				270			
acc	aag	atg	tcc	aat	gcc	acc	ctc	gtc	agc	tac	att	gtg	cag	atc	ctg	864
Thr	Lys	Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	Gln	Ile	Leu	
						275			280				285			
agc	cgc	tac	gac	atc	gcc	ctg	gtc	cag	gag	gtc	aga	gac	agc	cac	ctg	912
Ser	Arg	Tyr	Asp	Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	Asp	Ser	His	Leu	
						290			295				300			
act	gcc	gtg	ggg	aag	ctg	ctg	gac	aac	ctc	aat	cag	gac	gca	cca	gac	960
Thr	Ala	Val	Gly	Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	Asp	Ala	Pro	Asp	
						305			310				315			320
acc	tat	cac	tac	gtg	gtc	agt	gag	cca	ctg	gga	cg	aac	agc	tat	aag	1008
Thr	Tyr	His	Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	Asn	Ser	Tyr	Lys	
						325			330				335			
gag	cgc	tac	ctg	tcc	gtg	tac	agg	cct	gac	cag	gtg	tct	gcg	gtg	gac	1056
Glu	Arg	Tyr	Leu	Phe	Val	Tyr	Arg	Pro	Asp	Gln	Val	Ser	Ala	Val	Asp	
						340			345				350			
agc	tac	tac	tac	gat	gat	ggc	tgc	gag	ccc	tgc	ggg	aac	gac	acc	tcc	1104
Ser	Tyr	Tyr	Tyr	Asp	Asp	Gly	Cys	Glu	Pro	Cys	Gly	Asn	Asp	Thr	Phe	
						355			360				365			

aac cga gag cca gcc att gtc agg ttc ttc tcc cg <sup>g</sup> ttc aca gag gtc	1152
Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val	
370	375
380	
agg gag ttt gcc att gtt ccc ctg cat gcg gcc cc <sup>g</sup> ggg gac gca gta	1200
Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val	
385	390
395	400
gcc gag atc gac gct ctc tat gac gtc tac ctg gat gtc caa gag aaa	1248
Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys	
405	410
415	
tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc aat gcg ggc tgc	1296
Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys	
420	425
430	
agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc ctg tgg aca agc	1344
Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser	
435	440
445	
ccc acc ttc cag tgg ctg atc ccc gac agc gct gac acc aca gct aca	1392
Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr	
450	455
460	
ccc acg cac tgt gcc tat gac agg atc gtg gtt gca ggg atg ctg ctc	1440
Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu	
465	470
475	480
cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac ttc cag gct	1488
Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala	
485	490
495	
gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc agt gac cac tat	1536
Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr	
500	505
510	
cca gtg gag gtg atg ctg aag tga	1560
Pro Val Glu Val Met Leu Lys	
515	

&lt;210&gt; 76

&lt;211&gt; 519

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;400&gt; 76

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1	5
10	
15	

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 50 55 60

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn  
 65 70 80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn  
 85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
 115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240

Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro

245

250

255

Glu Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu  
 260 265 270

Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu  
 275 280 285

Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu  
 290 295 300

Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp  
 305 310 315 320

Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys  
 325 330 335

Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp  
 340 345 350

Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe  
 355 360 365

Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val  
 370 375 380

Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val  
 385 390 395 400

Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys  
 405 410 415

Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys  
 420 425 430

Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser  
 435 440 445

Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr  
 450 455 460

Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu  
 465 470 475 480

Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala  
 485 490 495

Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr  
 500 505 510

Pro Val Glu Val Met Leu Lys  
 515

<210> 77

<211> 1560

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 77		
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt ccactcccaag	60	
gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg gggcctcagt gaaggtgtcc	120	
tgcaggcctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180	
ggaaagggcc tcgagtggtt cgagagatt ttacctggaa gtaataattc tagataacaat	240	
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300	
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360	
tttgccttgtt ttgcttactg gggccaagg actctggtca cagtcctc caccctccacc	420	
aagggccat cggcttcccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480	
gccctggct gcctggcaa ggactacttc cccgaaccgg tgacgggtgc gtggactca	540	
ggcgccctga ccagcggcgt gcacaccccttc ccggctgtcc tacagtcctc aggactctac	600	
tccctcagca gcgtggtgac cgtccctcc agcagcttgg gcacccagac ctacatctgc	660	
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720	
gacaaaactc acacatgctg tgtggagtgc ccaccgtgcc cagcacctga aggcaggctg	780	
aagatcgcaag cttcaacat ccagacattt gggagacca agatgtccaa tgccaccctc	840	
gtcagctaca ttgtgcagat cctgagccgc tacgacatcg ccctggtcca ggaggtcaga	900	
gacagccacc tgactgccgt ggagaagctg ctggacaacc tcaatcagga cgcaccagac	960	

acctatcact acgtggtcag tgagccactg ggacggaaca gctataagga gcgctacctg 1020  
 ttcgtgtaca ggcctgacca ggtgtctgcg gtggacagct actactacga tcatggctgc 1080  
 gagccctgcg ggaacgacac cttcaaccga gagccagcca ttgtcagggtt cttctcccg 1140  
 ttcacagagg tcagggagtt tgccattgtt cccctgcattg cggccccggg ggacgcagta 1200  
 gccgagatcg acgctctcta tgacgtctac ctggatgtcc aagagaaatg gggcttggag 1260  
 gacgtcatgt tcatggcga cttcaatgcg ggctgcagct atgtgagacc ctcccagtgg 1320  
 tcatccatcc gcctgtggac aagccccacc ttccagtggc tcatccccga cagcgctgac 1380  
 accacagcta cacccacgca ctgtgcctat gacaggatcg tgggtgcagg gatgctgctc 1440  
 cgaggggccg ttgttcccga ctcggctt cccttaact tccaggctgc ctatggcctg 1500  
 agtaccaac tggcccaagc catcagtgac cactatccag tggaggtgat gctgaagtga 1560

&lt;210&gt; 78

&lt;211&gt; 1560

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

<400> 78  
 atgggatgga gctgttatcat ccttttttg gtagcaacag ctacaggtgt ccactccag 60  
 gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg gggcctcagt gaaggtgtcc 120  
 tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca 180  
 ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat 240  
 gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg 300  
 gagctcagca gcctgaggtc tgaggacaca gccgtctatt acttgcaag atcctacgac 360  
 ttgcctgggt ttgcttactg gggccaagg actctggtca cagtctcctc agcctccacc 420  
 aagggccat cggctttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 480  
 gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacgggtgc gtggactca 540  
 ggcgcctga ccagcggcgt gcacacccctc ccggctgtcc tacagtctc aggactctac 600  
 tccctcagca gcgtggtgac cgtccctcc agcagcttgg gcacccagac ctacatctgc 660  
 aacgtgaatc acaagccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 720

gacaaaactc acacatgctg tgcgttgtt ccaccgtgtc cagcaccaga gggcaggctg	780
aagatcgca cttcaacat ccagacattt ggggagacca agatgtccaa tgccaccctc	840
gtcagctaca ttgtgcagat cctgagccgc tacgacatcg ccctggtcca ggaggtcaga	900
gacagccacc tgactgccgt ggagaagctg ctggacaacc tcaatcagga cgccaccagac	960
acctatcact acgtggtcag tgagccactg ggacggaaca gctataagga gcgtacactg	1020
ttcgtgtaca ggcctgacca ggtgtctgctg gtggacagct actactacga tgcgtgtgc	1080
gagccctgctg ggaacgacac cttcaaccga gagccagcca ttgtcagggtt cttctcccg	1140
ttcacagagg tcagggagtt tgccattgtt cccctgcattg cggccccggg ggacgcagta	1200
gccgagatcg acgctctcta tgacgtctac ctggatgtcc aagagaaatg gggcttggag	1260
gacgtcatgt tgcgtggcga cttcaatgctg ggctgcagct atgtgagacc ctcccagtgg	1320
tcatccatcc gcctgtggac aagccccacc ttccagtggc tgcgtggc cagcgctgac	1380
accacagcta cacccacgca ctgtgcctat gacaggatcg tgggtgcagg gatgctgctc	1440
cgagggggccg ttgttcccgaa ctcggcttt cccttaact tccaggctgc ctatggcctg	1500
agtgaccaac tggcccaagc catcagtgac cactatccag tggaggtgat gctgaagtga	1560

<210> 79

<211> 1560

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<220>

<221> CDS

<222> (1)..(1560)

<223>

<400> 79

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt	48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1	5
	10
	15

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys 20 25 30	96
cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe 35 40 45	144
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu 50 55 60	192
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn 65 70 75 80	240
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn 85 90 95	288
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val 100 105 110	336
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly 115 120 125	384
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser 130 135 140	432
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala 145 150 155 160	480
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val 165 170 175	528
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 180 185 190	576
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 195 200 205	624
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 210 215 220	672
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 225 230 235 240	720
gac aaa act cac aca tgc tgt gtg gag tgc cca ccg tgc cca gca cct Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro 245 250 255	768

gaa ggc agg ctg aag atc gca gcc ttc aac atc cag aca ttt ggg gag Glu Gly Arg Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu 260 265 270	816
acc aag atg tcc aat gcc acc ctc gtc agc tac att gtg cag atc ctg Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu 275 280 285	864
agc cgc tac gac atc gcc ctg gtc cag gag gtc aga gac agc cac ctg Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu 290 295 300	912
act gcc gtg gag aag ctg ctg gac aac ctc aat cag gac gca cca gac Thr Ala Val Glu Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp 305 310 315 320	960
acc tat cac tac gtg gtc agt gag cca ctg gga cg <sup>g</sup> aac agc tat aag Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys 325 330 335	1008
gag cgc tac ctg ttc gtg tac agg cct gac cag gtg tct gc <sup>g</sup> gtg gac Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp 340 345 350	1056
agc tac tac tac gat gat ggc tgc gag ccc tgc ggg aac gac acc ttc Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe 355 360 365	1104
aac cga gag cca gcc att gtc agg ttc ttc tcc cgg ttc aca gag gtc Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val 370 375 380	1152
agg gag ttt gcc att gtt ccc ctg cat gc <sup>g</sup> gcc ccg ggg gac gca gta Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val 385 390 395 400	1200
gcc gag atc gac gct ctc tat gac gtc tac ctg gat gtc caa gag aaa Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys 405 410 415	1248
tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc aat gc <sup>g</sup> ggc tgc Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys 420 425 430	1296
agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc ctg tgg aca agc Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser 435 440 445	1344
ccc acc ttc cag tgg ctg atc ccc gac agc gct gac acc aca gct aca Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr 450 455 460	1392
ccc acg cac tgt gcc tat gac agg atc gtg gtt gca ggg atg ctg ctc Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu 465 470 475 480	1440
cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac ttc cag gct Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala	1488

485                  490                  495

gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc agt gac cac tat 1536  
 Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr  
                   500                  505                  510

cca gtg gag gtg atg ctg aag tga 1560  
Pro Val Glu Val Met Leu Lys  
515

<210> 80

<211> 519

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 80

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn  
65 70 75 80

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
115 120 125

## 120

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
225 230 235 240

Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro  
245 250 255

Glu Gly Arg Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu  
260 265 270

Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu  
275 280 285

Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu  
290 295 300

Thr Ala Val Glu Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp  
305 310 315 320

Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys  
325 330 335

Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp  
340 345 350

Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe  
355 360 365

Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val  
 370 375 380

Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val  
 385 390 395 400

Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys  
 405 410 415

Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys  
 420 425 430

Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser  
 435 440 445

Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr  
 450 455 460

Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu  
 465 470 475 480

Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala  
 485 490 495

Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr  
 500 505 510

Pro Val Glu Val Met Leu Lys  
 515

<210> 81

<211> 1578

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 81  
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tgcaaggctt	ctggctacac	cttcagtgcc	tactggatag	agtgggtgcg	ccaggctcca	180	
ggaaagggcc	tcgagtgggt	cggagagatt	ttacctggaa	gtaataattc	tagataacaat	240	
gagaagttca	agggccgagt	gacagtca	agagacacat	ccacaaacac	agcctacatg	300	
gagctcagca	gcctgaggtc	tgaggacaca	gccgtctatt	actgtgcaag	atcctacgac	360	
tttgccttgt	ttgcttactg	gggccaaggg	actctggta	cagtctcctc	agcctccacc	420	
aagggccat	cggtcttccc	cctggcaccc	tcctccaaga	gcacctctgg	gggcacagcg	480	
gccctggct	gcctggtaa	ggactacttc	cccgaaccgg	tgacgggtgc	gtggaactca	540	
ggcgccctga	ccagcggcgt	gcacaccc	ccggctgtcc	tacagtcc	aggactctac	600	
tccctcagca	gcgtggtgac	cgtgccctcc	agcagcttg	gcacccagac	ctacatctgc	660	
aacgtgaatc	acaagcccag	caacaccaag	gtggacaaga	aagttgagcc	caaatcttgt	720	
gacaaaactc	acacatgccc	accgtgccc	gcacctgaag	gcgggctgaa	gatcgagcc	780	
ttcaacatcc	agacatttg	ggagaccaag	atgtccatg	ccaccctcg	cagctacatt	840	
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actgccgtgg	ggaagctgct	ggacaaccc	aatcaggacg	caccagacac	ctatcactac	960	
gtggtcagtg	agccactggg	acggaacagc	tataaggac	gctacctgtt	cgtgtacagg	1020	
cctgaccagg	tgtctcggt	ggacagctac	tactacgtg	atggctgcga	gccctgcggg	1080	
aacgacacct	tcaaccgaga	gccagccatt	gtcaggttct	tctccgggt	cacagaggtc	1140	
agggagttg	ccattgttcc	cctgcatg	gccccgggg	acgcagtagc	cgagatcgac	1200	
gctctctatg	acgtctacct	ggatgtccaa	gagaaatggg	gcttggagga	cgtcatgtt	1260	
atgggcgact	tcaatgcggg	ctgcagctat	gtgagaccct	cccagtggtc	atccatccgc	1320	
ctgtggacaa	gccccaccc	ccagtggctg	atccccaca	gcgctgacac	cacagctaca	1380	
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gttcccga	cggctttcc	ctttaacttc	caggctgc	atggcctgag	tgaccaactg	1500	
gccccagcca	tca	gtgacca	ctatccagtg	gaggtgatgc	tgaaggggg	cgacccaaa	1560
aagaagcgca	agg	tttga				1578	

&lt;210&gt; 82

&lt;211&gt; 1578

&lt;212&gt; DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 82	
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt ccactccag	60
gtgcagctgg tgcagtctgg ggcagaggtg aaaaaggcctg gggcctcagt gaaggtgtcc	120
tgcaggcctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtggtt cgagagatt ttacctggaa gtaataattc tagataacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgcctgggt ttgcttactg gggccaaggg actctggtca cagtcctc tacccctccacc	420
aagggccat cggcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480
gccctggct gcctggcaa ggactacttc cccgaaccgg tgacgggtgc gtggactca	540
ggcgccctga ccagcggcgt gcacacccctc ccggctgtcc tacagtcctc aggactctac	600
tccctcagca gcgtggtgac cgtgcctcc agcagcttgg gcacccagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720
gacaaaactc acacatgtcc accgtgtcca gcaccagagg gcgggctgaa gatcgagcc	780
ttcaacatcc agacatttg ggagaccaag atgtccaatg ccaccctcgt cagctacatt	840
gtgcagatcc tgagccgcta cgacatcgcc ctggtccagg aggtcagaga cagccacctg	900
actgccgtgg ggaagctgct ggacaacctc aatcaggacg caccagacac ctatcactac	960
gtggtcagtg agccactggg acggaacacgc tataaggacg gctacctgtt cgtgtacagg	1020
cctgaccagg tgtctcggtt ggacagctac tactacgtg atggctgcga gccctgcggg	1080
aacgacacct tcaaccgaga gccagccatt gtcaggttct tctccgggtt cacagaggc	1140
agggagtttgc ccattgttcc cctgcatgct gccccgggg acgcagtagc cgagatcgac	1200
gctctctatg acgtctaccc ggtatgtccaa gagaaatggg gcttggagga cgtcatgtt	1260
atgggcact tcaatgcggg ctgcagctat gtgagaccct cccagtggtc atccatccgc	1320
ctgtggacaa gccccaccc ttccagtgatgctg atccccgaca gcgctgacac cacagctaca	1380
cccacgcact gtgcctatga caggatcgatg gttgcaggaa tgctgctccg agggccgtt	1440
gttcccgact cggctttcc ctttaacttc caggctgcct atggcctgag tgaccaactg	1500

gcccaaggcca tcagtgacca ctatccagtg gaggtgatgc tgaagggggg cggacccaa	1560
aagaagcgca aggtttga	1578
<210> 83	
<211> 1587	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Humanised HMFG1 Fd - DNase I fusion	
<400> 83	
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aagggtcct gcaaggcttc tggctacacc ttcatgtgcct actggataga gtgggtgcgc	180
caggctccag gaaaggcct cgagtggtc ggagagattt tacctggaag taataattct	240
agataacaatg agaagttcaa gggccgagtg acagtcacta gagacacatc cacaacaca	300
gcctacatgg agctcagcag cctgaggtct gaggacacag ccgtcttatta ctgtgcaaga	360
tcctacgact ttgcctggtt tgcttactgg ggccaaggga ctctggcac agtctcctca	420
gcctccacca agggccatc ggtttcccc ctggcaccct cctccaagag cacctctgg	480
ggcacagcgg ccctggctg cctggtcaag gactactcc ccgaaccggg gacggtgtcg	540
tggactcag gcccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca	600
ggactctact ccctcagcag cgtggtgacc gtgcctcca gcagttggg cacccagacc	660
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	720
aaatcttgtg acaaaaactca cacatgtcca ccgtgtccag caccagaggg cggctgaag	780
atcgccagcct tcaacatcca gacatttggg gagaccaaga tgtccaatgc caccctcg	840
agctacattg tgcagatct gagccgctac gacatcgccc tggtccagga ggtcagagac	900
agccacctga ctgccgtgg gaagctgctg gacaacctca atcaggacgc accagacacc	960
tatcactacg tggtcagtga gccactggga cggAACAGCT ataaggagcg ctacctgttc	1020
gtgtacaggc ctgaccaggc gtctgcggtg gacagctact actacgtga tggctgcgag	1080
ccctgcggga acgacacctt caaccgagag ccagccattg tcaggttctt ctcccggttc	1140
acagaggta gggagttgc cattgttccc ctgcattgcgg ccccgggggg cgcagtagcc	1200

gagatcgacg ctctcttatga cgtctacctg gatgtccaag agaaatgggg cttggaggac 1260  
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 tccatccgcc tgtggacaag ccccacccctc cagtggctga tccccgacag cgctgacacc 1380  
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 gggccgttg ttcccgactc ggctcttccc tttaacttcc aggctgccta tggcctgagt 1500  
 gaccaactgg cccaagccat cagtgaccac tatccagtgg aggtgatgct gaagggggc 1560  
 ggaccaaaaa agaagcgcaa ggtttga 1587

&lt;210&gt; 84

&lt;211&gt; 1578

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1578)

&lt;223&gt;

&lt;400&gt; 84

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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag	96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35 40 45	

agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc	192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
50 55 60	

gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat	240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn	

## 126

65	70	75	80	
				288
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac				
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn				
85	90	95		
				336
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc				
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val				
100	105	110		
				384
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc				
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly				
115	120	125		
				432
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg				
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser				
130	135	140		
				480
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg				
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala				
145	150	155	160	
				528
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg				
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val				
165	170	175		
				576
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct				
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala				
180	185	190		
				624
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc acc gtg				
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val				
195	200	205		
				672
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac				
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His				
210	215	220		
				720
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt				
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys				
225	230	235	240	
				768
gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ggc ggg ctg				
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Gly Gly Leu				
245	250	255		
				816
aag atc gca gcc ttc aac atc cag aca ttt ggg gag acc aag atg tcc				
Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys Met Ser				
260	265	270		
				864
aat gcc acc ctc gtc agc tac att gtg cag atc ctg agc cgc tac gac				
Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp				
275	280	285		
				912
atc gcc ctg gtc cag gag gtc aga gac agc cac ctg act gcc gtg ggg				
Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val Gly				
290	295	300		
				960
aag ctg ctg gac aac ctc aat cag gac gca cca gac acc tat cac tac				

Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	Asp	Ala	Pro	Asp	Thr	Tyr	His	Tyr		
305					310				315					320			
gtg	gtc	agt	gag	cca	ctg	gga	cgg	aac	agc	tat	aag	gag	cgc	tac	ctg	1008	
Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	Asn	Ser	Tyr	Lys	Glu	Arg	Tyr	Leu		
					325				330					335			
ttc	gtg	tac	agg	cct	gac	cag	gtg	tct	gcg	gtg	gac	agc	tac	tac	tac	1056	
Phe	Val	Tyr	Arg	Pro	Asp	Gln	Val	Ser	Ala	Val	Asp	Ser	Tyr	Tyr	Tyr		
					340				345					350			
gat	gat	ggc	tgc	gag	ccc	tgc	ggg	aac	gac	acc	ttc	aac	cga	gag	cca	1104	
Asp	Asp	Gly	Cys	Glu	Pro	Cys	Gly	Asn	Asp	Thr	Phe	Asn	Arg	Glu	Pro		
					355				360					365			
gcc	att	gtc	agg	ttc	tcc	cg	ttc	aca	gag	gtc	agg	gag	ttt	gcc		1152	
Ala	Ile	Val	Arg	Phe	Phe	Ser	Arg	Phe	Thr	Glu	Val	Arg	Glu	Phe	Ala		
					370				375					380			
att	gtt	ccc	ctg	cat	g	cc	gg	g	ac	g	ca	g	cc	g	atc	gac	1200
Ile	Val	Pro	Leu	His	Ala	Ala	Pro	Gly	Asp	Ala	Val	Ala	Glu	Ile	Asp		
					385				390					395		400	
gct	ctc	tat	gac	gtc	tac	ctg	gat	gtc	caa	gag	aaa	tgg	ggc	ttg	gag	1248	
Ala	Leu	Tyr	Asp	Val	Tyr	Leu	Asp	Val	Gln	Glu	Lys	Trp	Gly	Leu	Glu		
					405				410					415			
gac	gtc	atg	ttg	atg	ggc	gac	ttc	aat	g	cg	ggc	tgc	agc	tat	gtg	aga	1296
Asp	Val	Met	Leu	Met	Gly	Asp	Phe	Asn	Ala	Gly	Cys	Ser	Tyr	Val	Arg		
					420				425					430			
ccc	tcc	cag	tgg	tca	tcc	atc	cg	ctg	tgg	aca	agc	ccc	acc	ttc	cag	1344	
Pro	Ser	Gln	Trp	Ser	Ser	Ile	Arg	Leu	Trp	Thr	Ser	Pro	Thr	Phe	Gln		
					435				440					445			
tgg	ctg	atc	ccc	gac	agc	g	tc	gac	acc	aca	g	ct	ccc	ac	cac	tgt	1392
Trp	Leu	Ile	Pro	Asp	Ser	Ala	Asp	Thr	Thr	Ala	Thr	Pro	Thr	His	Cys		
					450				455					460			
gcc	tat	gac	agg	atc	gt	gt	gca	ggg	atg	ctg	ctc	cga	ggg	gcc	gtt	1440	
Ala	Tyr	Asp	Arg	Ile	Val	Val	Ala	Gly	Met	Leu	Leu	Arg	Gly	Ala	Val		
					465				470					475		480	
gtt	ccc	gac	tcg	g	ct	ccc	ttt	aa	ttc	cag	g	ct	gcc	tat	ggc	ctg	1488
Val	Pro	Asp	Ser	Ala	Leu	Pro	Phe	Asn	Phe	Gln	Ala	Ala	Tyr	Gly	Leu		
					485				490					495			
agt	gac	caa	ctg	gcc	caa	gcc	atc	agt	gac	cac	tat	cca	gt	gag	gt		1536
Ser	Asp	Gln	Leu	Ala	Gln	Ala	Ile	Ser	Asp	His	Tyr	Pro	Val	Glu	Val		
					500				505					510			
atg	ctg	aag	ggg	ggc	gga	ccc	aaa	aag	aag	cgc	aag	gtt	tga			1578	
Met	Leu	Lys	Gly	Gly	Gly	Pro	Lys	Lys	Lys	Arg	Lys	Val					
					515				520					525			

<211> 525

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 85

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
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Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn  
65 70 75 80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn  
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala

180	185	190
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val		
195	200	205
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His		
210	215	220
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys		
225	230	235
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Gly Gly Leu		
245	250	255
Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys Met Ser		
260	265	270
Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp		
275	280	285
Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val Gly		
290	295	300
Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His Tyr		
305	310	315
320		
Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr Leu		
325	330	335
Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr Tyr Tyr		
340	345	350
Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg Glu Pro		
355	360	365
Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu Phe Ala		
370	375	380
Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile Asp		
385	390	395
400		
Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu Glu		
405	410	415

## 130

Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg  
 420 425 430

Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln  
 435 440 445

Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr His Cys  
 450 455 460

Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly Ala Val  
 465 470 475 480

Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly Leu  
 485 490 495

Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val Glu Val  
 500 505 510

Met Leu Lys Gly Gly Pro Lys Lys Lys Arg Lys Val  
 515 520 525

<210> 86

<211> 1596

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 86

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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca 180

ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagataacaat 240

gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg 300

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tttgccttgtt ttgcttactg gggccaaggg actctggtca cagtcctc caccctccacc 420

aaggcccattt cggcttcccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 480

gccctggct	gcctggtcaa	ggactacttc	cccgaaccgg	tgacgggtgc	gtgaaactca	540
ggcgccctga	ccagcggcgt	gcacaccccttc	ccggctgtcc	tacagtccctc	aggactctac	600
tccctcagca	gcgtggtgac	cgtgccctcc	agcagcttgg	gcacccagac	ctacatctgc	660
aacgtgaatc	acaagcccag	caacaccaag	gtggacaaga	aagttgagcc	caaatcttgt	720
gacaaaactc	acacatgctg	tgtggagtgc	ccaccgtgcc	cagcacctga	aggagcggc	780
gggctgaaga	tcgcagcctt	caacatccag	acatttgggg	agaccaagat	gtccaatgcc	840
accctcgta	gctacattgt	gcagatcctg	agccgctacg	acatcgccct	ggtccaggag	900
gtcagagaca	gccacctgac	tgccgtgggg	aagctgctgg	acaaccta	tcaggacgca	960
ccagacacct	atcactacgt	ggtcagttag	ccactggac	ggaacagcta	taaggagcgc	1020
tacctgttcg	tgtacaggcc	tgaccaggtg	tctgcggtgg	acagctacta	ctacgatgat	1080
ggctgcgagc	cctgcggaa	cgacaccccttc	aaccgagagc	cagccattgt	caggttcttc	1140
tcccggttca	cagaggtcag	ggagtttgcc	attgttcccc	tgcattgcggc	cccgaaaaac	1200
gcagtagccg	agatcgacgc	tctctatgac	gtctacctgg	atgtccaaga	gaaatggggc	1260
ttggaggacg	tcatgttgat	ggcgacttc	aatgcggct	gcagctatgt	gagaccctcc	1320
cagtggtcat	ccatccgcct	gtggacaagc	cccaccccttc	agtggctgat	ccccgacagc	1380
gctgacacca	cagctacacc	cacgcactgt	gcctatgaca	ggatcgtgg	tgcaggatg	1440
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ggcctgagtg	accaactggc	ccaagccatc	agtgaccact	atccagtgga	ggtgatgctg	1560
aaggggggcg	gacccaaaaa	gaagcgcaag	gtttga			1596

&lt;210&gt; 87

&lt;211&gt; 1596

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;400&gt; 87

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gtgcagctgg	tgcagtctgg	ggcagaggtg	aaaaagcctg	gggcctcagt	gaaggtgtcc	120
tgcaaggctt	ctggctacac	cttcagtgcc	tactggatag	agtgggtgcg	ccaggctcca	180

ggaaagggcc tcgagtggtt cggagagatt ttacctggaa gtaataattc tagataacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggc tgaggacaca gccgtctatt acttgtcaag atcctacgac	360
tttgccttgtt ttgcttactg gggccaagg actctggtca cagtctcctc agcctccacc	420
aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480
gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacgggtgc gtggaactca	540
ggcgccctga ccagcggcgt gcacacccctc ccggctgtcc tacagtccctc aggactctac	600
tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720
gacaaaactc acacatgctg tgtcgagtgt ccaccgtgtc cagcaccaga ggggagcggc	780
gggctgaaga tcgcagcattt caacatccag acatttgggg agaccaagat gtccaatgcc	840
accctcgta gctacattgt gcagatcctg agccgctacg acatcgccct ggtccaggag	900
gtcagagaca gccacctgac tgccgtgggg aagctgctgg acaacctaattt tcaggacgca	960
ccagacacct atcactacgt ggtcagttag ccactggac ggaacagacta taaggagcgc	1020
tacctgttcg tgtacaggcc tgaccaggtg tctgcggtgg acagctacta ctacgatgat	1080
ggctgcgagc cctgcggaa cgacacccctc aaccgagagc cagccattgt caggttcttc	1140
tcccggttca cagaggtcag ggagttgcc attgttcccc tgcatgcggc cccgggggac	1200
gcagtagccg agatcgacgc tctctatgac gtctacctgg atgtccaaga gaaatggggc	1260
ttggaggacg tcatgttgat gggcgacttc aatgcgggct gcagctatgt gagaccctcc	1320
cagtggtcat ccatccgcct gtggacaagg cccacccctc agtggctgat ccccgacagc	1380
gctgacacca cagctacacc cacgcactgt gcctatgaca ggatcgtgg tgcaggatg	1440
ctgctccgag gggccgttgt tcccgactcg gctttccct ttaacttcca ggctgcctat	1500
ggcctgagtg accaactggc ccaagccatc agtgaccact atccagtgaa ggtgatgctg	1560
aaggggggcg gacccaaaaa gaagcgcaag gtttga	1596

&lt;210&gt; 88

&lt;211&gt; 1605

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

<400> 88	
gccgcccacca tggatggag ctgtatcatc ctcttcttgg tagcaacagc tacaggtgtc	60
cactcccagg tgcagctggt gcagtctgg gcagaggtga aaaagcctgg ggcctcagtg	120
aagggtgtcct gcaaggcttc tggctacacc ttcaagtgcct actggataga gtgggtgcgc	180
caggctccag gaaaggcct cgagtggtc ggagagattt tacctggaag taataattct	240
agataacaatg agaagttcaa gggccgagtg acagtcacta gagacacatc cacaacaca	300
gcctacatgg agctcagcag cctgaggtct gaggacacag ccgtcttatta ctgtgcaaga	360
tcctacgact ttgcctggtt tgcttactgg gccaaaggga ctctggtcac agtctcctca	420
gcctccacca agggccatc ggtttcccc ctggcacccct cctccaagag cacctctgg	480
ggcacagcgg ccctggctg cctggtcaag gactactcc ccgaaccgggt gacggtgtcg	540
tggaaactcag ggccttgac cagcggcgtg cacacccctcc cggctgtcct acagtcctca	600
ggactctact ccctcagcag cgtggtgacc gtgcctcca gcagcttggg cacccagacc	660
tacatctgca acgtaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	720
aaatcttgtg acaaaaactca cacatgctgt gtcgagtgtc caccgtgtcc agcaccagag	780
gggagcggcg ggctgaagat cgccgccttc aacatccaga catttgggg gaccaagatg	840
tccaatgcca ccctcgtag ctacattgtg cagatcctga gccgctacga catcgccctg	900
gtccaggagg tcagagacag ccacctgact gccgtgggg agctgctgga caacctaat	960
caggacgcac cagacaccta tcactacgtg gtcagtgagc cactggacg gaacagctat	1020
aaggagcgct acctgttcgt gtacaggcct gaccaggtgt ctgcggtgga cagctactac	1080
tacgatgatg gtcgagcc ctgcggAAC gacacccatca accgagagcc agccattgtc	1140
agtttttttcccggttcac agaggtcagg gagttgcca ttgttccct gcatgcggcc	1200
ccggggggacg cagtagccga gatcgacgct ctctatgacg tctacctgga tgtccaagag	1260
aaatggggct tggaggacgt catgttcatg ggcgacttca atgcggctg cagctatgt	1320
agaccctccc agtggtcatc catccgcctg tggacaagcc ccacccatca gtggctgatc	1380
cccgacagcg ctgacaccac agctacaccc acgcactgtg cctatgacag gatcggtt	1440
gcagggatgc tgctccgagg ggccgttggt cccgactcgg ctctccctt taacttccag	1500
gctgcctatg gcctgagtga ccaactggcc caagccatca gtgaccacta tccagtgag	1560

gtgatgctga aggggggcgg acccaaaaag aagcgcaagg tttga 1605

<210> 89

<211> 1596

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<220>

<221> CDS

<222> (1)..(1596)

<223>

<400> 89

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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag 96

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc 144

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35 40 45	

agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc 192

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
50 55 60	

gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat 240

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn	
65 70 75 80	

gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac 288

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn	
85 90 95	

aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc 336

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
100 105 110	

tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc 384

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly	
115 120 125	

caa	ggg	act	ctg	gtc	aca	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg		432
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser		
130					135							140					
gtc	tcc	ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg		480
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala		
145					150					155				160			
gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	tcc	ccc	gaa	ccg	gtg	acg	gtg		528
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val		
					165				170				175				
tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct		576
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala		
					180				185				190				
gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg		624
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Val	Thr	Val	
					195				200			205					
ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac		672
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His		
					210				215			220					
aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt		720
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys		
					225				230			235			240		
gac	aaa	act	cac	aca	tgc	tgt	gtg	gag	tgc	cca	ccg	tgc	cca	gca	cct		768
Asp	Lys	Thr	His	Thr	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro		
					245				250			255					
gaa	ggg	agc	ggc	ggg	ctg	aag	atc	gca	gcc	ttc	aac	atc	cag	aca	ttt		816
Glu	Gly	Ser	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	Thr	Phe		
					260				265			270					
ggg	gag	acc	aag	atg	tcc	aat	gcc	acc	ctc	gtc	agc	tac	att	gtg	cag		864
Gly	Glu	Thr	Lys	Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	Gln		
					275				280			285					
atc	ctg	agc	cgc	tac	gac	atc	gcc	ctg	gtc	cag	gag	gtc	aga	gac	agc		912
Ile	Leu	Ser	Arg	Tyr	Asp	Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	Asp	Ser		
					290				295			300					
cac	ctg	act	gcc	gtg	ggg	aag	ctg	ctg	gac	aac	ctc	aat	cag	gac	gca		960
His	Leu	Thr	Ala	Val	Gly	Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	Asp	Ala		
					305				310			315			320		
cca	gac	acc	tat	cac	tac	gtg	gtc	agt	gag	cca	ctg	gga	cg	aac	agc		1008
Pro	Asp	Thr	Tyr	His	Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	Asn	Ser		
					325				330			335					
tat	aag	gag	cgc	tac	ctg	ttc	gtg	tac	agg	cct	gac	cag	gtg	tct	gcg		1056
Tyr	Lys	Glu	Arg	Tyr	Leu	Phe	Val	Tyr	Arg	Pro	Asp	Gln	Val	Ser	Ala		
					340				345			350					
gtg	gac	agc	tac	tac	tac	gat	gat	ggc	tgc	gag	ccc	tgc	ggg	aac	gac		1104
Val	Asp	Ser	Tyr	Tyr	Tyr	Asp	Asp	Gly	Cys	Glu	Pro	Cys	Gly	Asn	Asp		

355	360	365	
acc ttc aac cga gag cca gcc att gtc agg ttc ttc tcc cg <sup>g</sup> ttc aca Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr 370	375	380	1152
gag gtc agg gag ttt gcc att gtt ccc ctg cat gc <sup>g</sup> gcc cc <sup>g</sup> ggg gac Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp 385	390	395	1200
gca gta gcc gag atc gac gct ctc tat gac gtc tac ctg gat gtc caa Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln 405	410	415	1248
gag aaa tgg ggc ttg gag gac gtc atg ttg atg ggc gac tt <sup>c</sup> aat gc <sup>g</sup> Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala 420	425	430	1296
ggc tgc agc tat gtg aga ccc tcc cag tgg tca tcc atc cg <sup>c</sup> ctg tgg Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp 435	440	445	1344
aca agc ccc acc ttc cag tgg ctg atc ccc gac agc gct gac acc aca Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr 450	455	460	1392
gct aca ccc acg cac tgt gcc tat gac agg atc gtg gtt gca ggg atg Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met 465	470	475	1440
ctg ctc cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac tt <sup>c</sup> Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe 485	490	495	1488
cag gct gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc agt gac Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp 500	505	510	1536
cac tat cca gtg gag gtg atg ctg aag ggg ggc gga ccc aaa aag aag His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Pro Lys Lys Lys 515	520	525	1584
cg <sup>c</sup> aag gtt tga Arg Lys Val 530			1596

&lt;210&gt; 90

&lt;211&gt; 531

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 90

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1				5					10				15		

Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
								25					30		

Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
							40					45			

Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
					55				60						

Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn
65				70					75				80		

Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn
					85			90				95			

Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val
			100					105				110			

Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly
						115		120			125				

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
						130		135			140				

Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala
145					150				155			160			

Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
						165			170				175		

Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
						180		185			190				

Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
						195		200			205				

Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His
						210		215			220				

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225                    230                    235                    240

Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro  
 245                    250                    255

Glu Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe  
 260                    265                    270

Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln  
 275                    280                    285

Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser  
 290                    . 295                    300

His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala  
 305                    310                    315                    320

Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser  
 325                    330                    335

Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala  
 340                    345                    350

Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp  
 355                    360                    365

Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr  
 370                    375                    380

Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp  
 385                    390                    395                    400

Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln  
 405                    410                    415

Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala  
 420                    425                    430

Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp  
 435                    440                    445

Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr  
 450                    455                    460

Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met  
 465 470 475 480

Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe  
 485 490 495

Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp  
 500 505 510

His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Pro Lys Lys Lys  
 515 520 525

Arg Lys Val  
 530

<210> 91

<211> 1590

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 91	
atgggatgga gctgttatcat cctcttcttg gtagcaacag ctacaggtgt ccactcccaag	60
gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg gggcctcagt gaagggtgtcc	120
tgcaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagataaat	240
gagaagttca agggccgagt gacagtcaact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgcctggc ttgcttactg gggccaagg actctggtca cagtctcctc agcctccacc	420
aaggggccat cggctttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480
gccctggct gcctggtcaa ggactacttc cccgaaccgg tgacgggtgc gtggaaactca	540
ggcgccctga ccagcggcgt gcacacccctc ccggctgtcc tacagtccctc aggactctac	600
tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	660

aacgtgaatc acaagcccag caacacccaag gtggacaaga aagttaggcc caaatcttgt	720
gacaaaactc acacatgctg tgtggagtgc ccaccgtgcc cagcacctga aggcgggctg	780
aagatcgca gcttcaacat ccagacattt ggggagacca agatgtccaa tgccaccctc	840
gtcagctaca ttgtgcagat cctgagccgc tacgacatcg ccctggtcca ggaggtcaga	900
gacagccacc tgactgccgt gggaaagctg ctggacaacc tcaatcagga cgaccacagac	960
acctatcact acgtggtcag tgagccactg ggacggaaca gctataagga gcgcgtacctg	1020
ttcgtgtaca ggcctgacca ggtgtctgcg gtggacagct actactacga tcatggctgc	1080
gagccctgcg ggaacgacac cttcaaccga gagccagcca ttgtcaggtt cttctcccg	1140
ttcacagagg tcagggagtt tgccattgtt cccctgcatt cgccccggg ggacgcagta	1200
gccgagatcg acgctctcta tgacgtctac ctggatgtcc aagagaaatg gggcttggag	1260
gacgtcatgt tcatggcga cttcaatgcg ggctgcagct atgtgagacc ctcccagtgg	1320
tcatccatcc gcctgtggac aagccccacc ttccagtggc tcatccccga cagcgctgac	1380
accacagcta cacccacgca ctgtgcctat gacaggatcg tgggtgcagg gatgctgctc	1440
cgagggggccg ttgttcccga ctggctctt cccttaact tccaggctgc ctatggcctg	1500
agtgaccaac tggcccaagc catcagtgac cactatccag tggaggtgat gctgaagggg	1560
ggcggaccca aaaagaagcg caaggttga	1590

<210> 92

<211> 1590

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 92 atgggatgga gctgttatcat ccttttttg gtagcaacag ctacaggtgt ccactccca	60
gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg gggcctcagt gaagggtgtcc	120
tgcaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat	240
gagaagtca agggccgagt gacagtact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggc tgaggacaca gccgtctatt acttgcaag atcctacgac	360

tttgcctgg	ttgcttactg	ggccaagg	actctggtca	cagtctc	agcctccacc	420	
aaggccc	cggtcttccc	cctggcaccc	tcctccaaga	gcac	ttctgg	ggcacagcg	480
gccctgg	gcctggtaa	ggactacttc	cccgaaccgg	tgacgg	gtgg	actca	540
ggcgcc	ccagcggcgt	gcacac	ccggctgtcc	tacag	tc	aggactctac	600
tccctc	agca	gcgtgg	cg	tgcc	ttgg	gcacccagac	660
aacgtgaatc	acaagcccag	caacaccaag	gtggaca	aagttgag	ccaa	atcttgt	720
gacaaaactc	acacatgctg	tgtcgagtgt	ccaccgt	tc	agcacc	gggggg	780
aagatcg	cattcaacat	ccagacattt	ggggagacca	agatgt	ccaa	tgccacc	840
gtcagctaca	ttgtgcagat	cctgagccgc	tacgacatcg	cc	ctgg	tcca	900
gacagccacc	tgactg	ccccgt	ggggaa	ctg	ctggaca	acc	960
acctatcact	acgtgg	tcag	tgagcc	actg	tc	ataagga	1020
ttcgtgtaca	ggc	ctgacca	ggtgt	ctgc	gtgg	act	1080
gagcc	ctg	cg	ggag	ctg	tc	actacga	1140
ttcacagagg	tcagg	agg	ttcatt	gtt	cc	atcg	1200
gccgagatcg	acg	ctct	tc	tgacgt	tc	ttgg	1260
tcatccatcc	gc	ctgtgg	ac	ttcc	actgg	ttgg	1320
accacagcta	cacccac	cgca	ctgtgc	cctat	gacagg	atcg	1380
cgagggccg	ttgttccc	ga	ctcg	ctt	atcc	ttgg	1440
agtgaccaac	tggccc	aa	cc	taact	tccagg	ctgc	1500
ggcggaccca	aaa	aga	agg	cg	gt	gaagg	1560
							1590

&lt;210&gt; 93

&lt;211&gt; 1599

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;400&gt; 93

gccgccacca	tggatggag	ctgtatcatc	ctcttcttgg	tagcaacagc	tacaggtgtc	60
cactcccagg	tgtagctgg	gcagtctggg	gcagaggtga	aaaagcctgg	ggcctcagtg	120
aagggtcct	gcaaggcttc	tggctacacc	ttcagtgcct	actggataga	gtgggtgcgc	180
caggctccag	gaaagggcct	cgagtggtc	ggagagattt	tacctggaag	taataattct	240
agataacaatg	agaagttcaa	ggcccgagtg	acagtcacta	gagacacatc	cacaaacaca	300
gcctacatgg	agctcagcag	cctgaggtct	gaggacacag	ccgtcttatta	cttgcaaga	360
tcctacgact	ttgcctgg	tgcttactgg	ggccaaggga	ctctggtcac	agtctcctca	420
gcctccacca	agggccatc	ggtttcccc	ctggcaccct	cctccaagag	cacctctgg	480
ggcacagcgg	ccctggctg	cctggtcaag	gactactcc	ccgaaccgg	gacggtgtcg	540
tggaaactcag	gcgcctgac	cagcggcgtg	cacacctcc	cggctgtcct	acagtcctca	600
ggactctact	ccctcagcag	cgtggtgacc	gtgcctcca	gcagttgg	cacccagacc	660
tacatctgca	acgtaatca	caagcccagc	aacaccaagg	tggacaagaa	agttgagccc	720
aaatcttgt	acaactca	cacatgtgt	gtcgagtgtc	caccgtgtcc	agcaccagag	780
ggcgggctga	agatcgcagc	cttcaacatc	cagacattt	ggagaccaa	gatgtccaa	840
gccaccctcg	ttagtacat	tgtcagatc	ctgagccgct	acgacatcgc	cctggtccag	900
gaggtcagag	acagccacct	gactgccgtg	ggaaagctgc	tggacaacct	caatcaggac	960
gcaccagaca	cctatcacta	cgtggtcagt	gagccactgg	gacgaaacag	ctataaggag	1020
cgttacctgt	tcgtgtacag	gcctgaccag	gtgtctgcgg	tggacagcta	ctactacgt	1080
gatggctg	agccctgcgg	gaacgacacc	ttcaaccgag	agccagccat	tgtcaggttc	1140
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gacgcagtag	ccgagatcga	cgctcttat	gacgtctacc	tggatgtcca	agagaaatgg	1260
ggcttgagg	acgtcatgtt	gatggcgac	ttcaatgcgg	gctgcagcta	tgtgagaccc	1320
tcccagtgg	catccatccg	cctgtggaca	agccccacct	tccagtggct	gatccccgac	1380
agcgctgaca	ccacagctac	acccacgcac	tgtgcctatg	acaggatcgt	ggttgcaggg	1440
atgctgctcc	gagggccgt	tgttcccgac	tcggcttcc	ccttaactt	ccaggctgcc	1500
tatggcctga	gtgaccaact	ggcccaagcc	atcagtgacc	actatccagt	ggaggtgatg	1560
ctgaaggggg	gcggacccaa	aaagaagcgc	aaggtttga			1599

&lt;210&gt; 94

&lt;211&gt; 1590

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<220>

<221> CDS

<222> (1)..(1590)

<223>

<400> 94

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atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1           5                   10                  15

```

48

96

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc  
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45

144

192

gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat  
 Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn  
 65 70 75 80

240

gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac  
 Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn  
                   85                  90                  95

288

aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc  
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
                   100                  105                  110

336

tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc  
 Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
 115                    120                    125

384

caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg  
 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 130 135 140

432

145	150	155	160	
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val	165	170	175	528
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala	180	185	190	576
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val	195	200	205	624
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His	210	215	220	672
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys	225	230	235	720
gac aaa act cac aca tgc tgt gtg gag tgc cca ccg tgc cca gca cct Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro	245	250	255	768
gaa ggc ggg ctg aag atc gca gcc ttc aac atc cag aca ttt ggg gag Glu Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu	260	265	270	816
acc aag atg tcc aat gcc acc ctc gtc agc tac att gtg cag atc ctg Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu	275	280	285	864
agc cgc tac gac atc gcc ctg gtc cag gag gtc aga gac agc cac ctg Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu	290	295	300	912
act gcc gtg ggg aag ctg ctg gac aac ctc aat cag gac gca cca gac Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp	305	310	315	960
acc tat cac tac gtg gtc agt gag cca ctg gga cgg aac agc tat aag Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys	325	330	335	1008
gag cgc tac ctg ttc gtg tac agg cct gac cag gtg tct gcg gtg gac Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp	340	345	350	1056
agc tac tac tac gat gat ggc tgc gag ccc tgc ggg aac gac acc ttc Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe	355	360	365	1104
aac cga gag cca gcc att gtc agg ttc ttc tcc cgg ttc aca gag gtc Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val	370	375	380	1152
agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg gac gca gta				1200

<210> 95  
<211> 529  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Humanised HMFG1 Fd - DNase I fusion  
<400> 95

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 50 55 60

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn  
 65 70 75 80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn  
 85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
 115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240

Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro  
 245 250 255

Glu Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu  
 260 265 270

Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu  
 275 280 285

Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu  
 290 295 300

Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp  
 305 310 315 320

Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys  
 325 330 335

Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp  
 340 345 350

Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe  
 355 360 365

Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val  
 370 375 380

Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val  
 385 390 395 400

Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys  
 405 410 415

Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys  
 420 425 430

Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser  
 435 440 445

Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr  
 450 455 460

Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu  
 465 470 475 480

Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala

148

485

490

495

Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr  
500 505 510

Pro Val Glu Val Met Leu Lys Gly Gly Pro Lys Lys Lys Arg Lys  
515 520 525

Val

<210> 96

<211> 7

<212> PRT

<213> Simian virus 40

<400> 96

Pro Lys Lys Lys Arg Lys Val  
1 5

<210> 97

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 97

Gly Ser Gly Gly  
1

<210> 98

<211> 9

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Consensus ribosome binding sequence

&lt;400&gt; 98

gccccccacc

9

&lt;210&gt; 99

&lt;211&gt; 35

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Fusion protein

&lt;400&gt; 99

Pro	Asp	Thr	Arg	Pro	Pro	Asp	Thr	Arg	Pro	Pro	Asp	Thr	Arg	Pro	Pro
1				5					10				15		

Asp	Thr	Arg	Pro	Pro	Asp	Thr	Arg	Pro	Pro	Asp	Thr	Arg	Pro	Pro	Asp
			20					25				30			

Thr	Arg	Pro
	35	

&lt;210&gt; 100

&lt;211&gt; 12

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Variant hinge

&lt;400&gt; 100

Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu
1				5				10			

150

<210> 101

<211> 5

<212> PRT

A<sup>35</sup>  
act <213> Homo sapiens

<400> 101

Ala Pro Asp Thr Arg  
1 5